



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 153501

TO: Terra Gibbs
Location: REM-2D10&2C18
Art Unit: 1635
Wednesday, May 25, 2005

Case Serial Number: 10/018437

From: Toby Port
Location: Biotech-Chem Library
REM1-A59
Phone: 272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Gibbs,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact **the searcher or contact:**

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



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153501

From: Gibbs, Terra
Sent: Monday, May 16, 2005 11:16 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search request...

Please perform a search of SEQ ID NO:3 of USSN 10/018,437 in all commercial databases, pending files, and pre-grant pubs.

Please perform this search as:

- a) a regular search for any sequences comprising SEQ ID NO:2 and
- b) a length limited search wherein the length of the oligo hits is limited to less than 50 nucleotides in length.

Terra Cotta Gibbs, Ph.D.
Art Unit 1635
Remsen Building 2D10
Mailbox 2C18
571-272-0758

CRF

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MAY 16 2005
STIC

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Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 04:25:28 ; Search time 1821 Seconds
(without alignments)
532.182 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacggagcgggaugccuu 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 750 summaries

Database:

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX045382 Sequence
2	20	100.0	20	6	AX045383 Sequence
3	20	100.0	623	6	AR365528 Sequence
4	20	100.0	661	6	AX525911 Sequence
5	20	100.0	686	4	AB116145 Canis fam
6	20	100.0	708	10	U34964 Rattus norv
7	20	100.0	711	4	AY509563 Canis fam
8	20	100.0	711	6	AR487796 Sequence
9	20	100.0	711	6	AX708370 Sequence
10	20	100.0	711	10	AF512835 Rattus no
11	20	100.0	717	6	AR052622 Sequence
12	20	100.0	717	6	BD187535 REGULATIO
13	20	100.0	720	6	CQ881810 Sequence
14	20	100.0	720	6	E49812 apoptosis-i
15	20	100.0	720	6	E49813 apoptosis-i
16	20	100.0	720	6	E49814 apoptosis-i
17	20	100.0	720	6	E49815 apoptosis-i
18	20	100.0	720	6	E49816 apoptosis-i
19	20	100.0	720	6	BD094977 Apoptosis

20	20	100.0	720	6	BD094978	BD094978 Apoptosis
21	20	100.0	720	6	BD094979	BD094979 Apoptosis
22	20	100.0	720	6	BD094980	BD094980 Apoptosis
23	20	100.0	720	6	BD094981	BD094981 Apoptosis
24	20	100.0	760	6	AR021160	AR021160 Sequence
25	20	100.0	765	6	A76121	A76121 Sequence 1
26	20	100.0	771	6	E58776	E58776 Screening m
27	20	100.0	953	6	E23358	E23358 Virus vecto
28	20	100.0	1179	10	RATBCL2A	L14680 Rattus norv
29	20	100.0	1374	4	AB154172	AB154172 Canis fam
30	20	100.0	1423	4	AB096611	AB096611 Felis cat
31	20	100.0	1846	6	AR054009	AR054009 Sequence
32	20	100.0	1846	6	AR146185	AR146185 Sequence
33	20	100.0	1846	9	HSBCL2IG	X06487 H.sapiens m
34	20	100.0	2704	6	CQ769647	CQ769647 Sequence
35	20	100.0	2704	9	BC027258	BC027258 Homo sapi
36	20	100.0	4825	6	AR365070	AR365070 Sequence
37	20	100.0	5086	6	AR052621	AR052621 Sequence
38	20	100.0	5086	6	AR054008	AR054008 Sequence
39	20	100.0	5086	6	AR146184	AR146184 Sequence
40	20	100.0	5086	6	BD187534	BD187534 REGULATIO
41	20	100.0	5086	6	AR237427	AR237427 Sequence
42	20	100.0	5086	6	BD008997	BD008997 Inhibitio
43	20	100.0	5086	6	BD084821	BD084821 Diagnosis
44	20	100.0	5086	9	HUMBCL2A	M13994 Human B-cel
45	20	100.0	5104	6	AX277471	AX277471 Sequence
46	20	100.0	5104	6	AR365527	AR365527 Sequence
47	20	100.0	5105	6	I08038	I08038 Sequence 1
48	20	100.0	6030	6	CQ827861	CQ827861 Sequence
49	20	100.0	6030	6	AR380470	AR380470 Sequence
50	20	100.0	6030	6	AX587647	AX587647 Sequence
51	20	100.0	6030	6	AX774854	AX774854 Sequence
52	20	100.0	6030	9	HUMBCL2C	M14745 Human bcl-2
53	20	100.0	6032	6	AX057146	AX057146 Sequence
54	20	100.0	7996	6	E23359	E23359 Virus vecto
55	18.4	92.0	20	6	AX045385	AX045385 Sequence
56	18.4	92.0	201	4	AF512029	AF512029 Cervus el
57	18.4	92.0	687	4	BTU92434	U92434 Bos taurus
58	18.4	92.0	2228	5	GDPCKBCL2	Z11961 G.domesticu
59	18.4	92.0	114253	9	AC091731	AC091731 Homo sapi
60	18.4	92.0	119160	2	AC135533	AC135533 Rattus no
61	18.4	92.0	192898	9	AC145968	AC145968 Pan trogl
62	18.4	92.0	244594	2	AC112470	AC112470 Rattus no
63	18.4	92.0	245229	2	AC099093	AC099093 Rattus no
64	17.4	87.0	154413	9	AC021989	AC021989 Homo sapi
65	17.4	87.0	157810	2	AC010813	AC010813 Homo sapi
66	17.4	87.0	172576	9	CNS01DSG	AL121775 Human chr
67	17.4	87.0	177862	9	AC068812	AC068812 Homo sapi
68	17	85.0	171868	9	AL359697	AL359697 Human DNA
69	17	85.0	194873	2	AL592440	AL592440 Homo sapi
70	16.8	84.0	379	6	AR379887	AR379887 Sequence
71	16.8	84.0	711	10	AF404339	AF404339 Cricetulu
72	16.8	84.0	902	10	CL0271720	AJ271720 Cricetulu
73	16.8	84.0	950	6	AR220790	AR220790 Sequence
74	16.8	84.0	1154	6	AR542085	AR542085 Sequence
75	16.8	84.0	1338	5	BC074505	BC074505 Xenopus t
76	16.8	84.0	1434	1	AY208890	AY208890 Vibrio fu
77	16.8	84.0	1704	6	CQ741478	CQ741478 Sequence
78	16.8	84.0	1764	10	HAMP450	M27906 Hamster maj
79	16.8	84.0	1771	10	HAMCP41	M63788 Hamster cys
80	16.8	84.0	2192	9	BC028012	BC028012 Homo sapi
81	16.8	84.0	2206	6	CQ611046	CQ611046 Sequence
82	16.8	84.0	2208	10	AF304364	AF304364 Rattus no
83	16.8	84.0	2361	9	HSA272324	AJ272324 Homo sapi
84	16.8	84.0	2797	3	AY058748	AY058748 Drosophila
85	16.8	84.0	4206	6	CQ611045	CQ611045 Sequence
86	16.8	84.0	7017	14	AF296093	AF296093 Porcine t
87	16.8	84.0	17089	2	AC019936	AC019936 Drosophila
88	16.8	84.0	41131	2	AC091480	Continuation (7 of
89	16.8	84.0	43715	9	AC092298	AC092298 Homo sapi
90	16.8	84.0	47812	9	HS127L4	283839 Human DNA s
91	16.8	84.0	74932	9	AC008762	AC008762 Homo sapi
92	16.8	84.0	82179	2	AC100650	AC100650 Mus muscu

c 93	16.8	84.0	91383	3	AE003572	Drosophil	166	16.4	82.0	252587	2	AC137203	Rattus no
c 94	16.8	84.0	110000	2	AC098332	Continuation (3 of	c 167	16.4	82.0	266597	2	AC119722	Rattus no
c 95	16.8	84.0	118561	2	AC09217	AC09217 Drosophil	c 168	16.4	82.0	321049	2	AC137221	Rattus no
c 96	16.8	84.0	118773	8	AF541963	Glycine m	c 169	16	80.0	601	11	BV167592	BV167592 sqm5976
c 97	16.8	84.0	143043	2	AC151842	AC151842 Mus muscu	170	16	80.0	1901	6	E31258	E31258 Liver-speci
c 98	16.8	84.0	143350	2	AC121509	AC121509 Mus muscu	171	16	80.0	1901	6	E31259	E31259 Liver-speci
c 99	16.8	84.0	149546	9	AC087256	AC087256 Homo sapi	172	16	80.0	1910	10	RATLSTP	L27651 Rattus norv
c 100	16.8	84.0	168227	9	AC021868	AC021868 Homo sapi	173	16	80.0	7453	10	RATLIVTR	L30107 Rattus norv
c 101	16.8	84.0	169128	8	AP005864	AP005864 Oryza sat	c 174	16	80.0	73704	2	AC064804	AC064804 Homo sapi
c 102	16.8	84.0	170975	3	AC011705	AC011705 Drosophil	c 175	16	80.0	79470	2	AL391000	AL391000 Homo sapi
c 103	16.8	84.0	173656	10	AC135113	AC135113 Mus muscu	c 176	16	80.0	80099	2	AC021290	AC021290 Homo sapi
c 104	16.8	84.0	180035	2	AC125819	AC125819 Rattus no	c 177	16	80.0	94063	2	AC137312	AC137312 Rattus no
c 105	16.8	84.0	183769	2	AC150884	AC150884 Bos tauru	c 178	16	80.0	109056	2	AC074053	AC074053 Homo sapi
c 106	16.8	84.0	183936	10	AC132921	AC132921 Mus muscu	c 179	16	80.0	136236	2	AL132068	AL132068 Rattus no
c 107	16.8	84.0	192658	2	AC132225	AC132225 Mus muscu	c 180	16	80.0	145673	2	AL391068	AL391068 Homo sapi
c 108	16.8	84.0	194490	10	AL845309	AL845309 Mouse DNA	c 181	16	80.0	151202	9	AL160168	AL160168 Human DNA
c 109	16.8	84.0	196817	9	AC019209	AC019209 Homo sapi	c 182	16	80.0	152626	2	AL357252	AL357252 Homo sapi
c 110	16.8	84.0	197019	9	AL157938	AL157938 Human DNA	c 183	16	80.0	157575	9	AL355520	AL355520 Human DNA
c 111	16.8	84.0	211414	10	AC104885	AC104885 Mus muscu	c 184	16	80.0	158470	2	AC009026	AC009026 Homo sapi
c 112	16.8	84.0	214292	10	AC084163	AC084163 Mus muscu	c 185	16	80.0	158801	2	AC147205	AC147205 Xenopus t
c 113	16.8	84.0	220057	2	AC098380	AC098380 Rattus no	c 186	16	80.0	161099	10	AC132624	AC132624 Mus muscu
c 114	16.8	84.0	222932	2	AC137869	AC137869 Mus muscu	c 187	16	80.0	161988	2	AC009129	AC009129 Homo sapi
c 115	16.8	84.0	226299	2	AC112320	AC112320 Rattus no	c 188	16	80.0	167322	2	AC147210	AC147210 Xenopus t
c 116	16.8	84.0	228520	2	AC118484	AC118484 Rattus no	c 189	16	80.0	167429	9	AC110771	AC110771 Homo sapi
c 117	16.8	84.0	241627	2	AC128374	AC128374 Rattus no	c 190	16	80.0	168083	9	AC092376	AC092376 Homo sapi
c 118	16.8	84.0	244292	2	AC098749	AC098749 Rattus no	c 191	16	80.0	175222	2	AC130641	AC130641 Rattus no
c 119	16.8	84.0	249747	2	AC094736	AC094736 Rattus no	c 192	16	80.0	176408	2	AC148598	AC148598 Xenopus t
c 120	16.8	84.0	258818	2	AC135265	AC135265 Rattus no	c 193	16	80.0	179417	2	AC009138	AC009138 Homo sapi
c 121	16.8	84.0	260131	2	AC128411	AC128411 Rattus no	c 194	16	80.0	193261	9	AC025281	AC025281 Homo sapi
c 122	16.8	84.0	260335	2	AC115140	AC115140 Rattus no	c 195	16	80.0	194593	10	AC116470	AC116470 Mus muscu
c 123	16.8	84.0	260367	2	AC099427	AC099427 Rattus no	c 196	16	80.0	201387	2	AC026565	AC026565 Homo sapi
c 124	16.8	84.0	276234	2	AC112380	AC112380 Rattus no	c 197	16	80.0	202508	2	AC114610	AC114610 Mus muscu
c 125	16.8	84.0	287560	1	AE017274	AE017274 Bacillus	c 198	16	80.0	203681	2	AC122079	AC122079 Rattus no
c 126	16.8	84.0	300658	1	AE017313	AE017313 Desulfovi	c 199	16	80.0	203964	10	AC122233	AC122233 Mus muscu
c 127	16.4	82.0	667	1	AB164137	AB164137 Unculture	c 200	16	80.0	206121	2	AC122362	AC122362 Mus muscu
c 128	16.4	82.0	692	1	AB164084	AB164084 Unculture	c 201	16	80.0	206231	9	AL592309	AL592309 Human DNA
c 129	16.4	82.0	727	1	AB164086	AB164086 Unculture	c 202	16	80.0	207105	2	AC123332	AC123332 Rattus no
c 130	16.4	82.0	738	13	AF548987	AF548987 Unculture	c 203	16	80.0	208207	9	AC022164	AC022164 Homo sapi
c 131	16.4	82.0	756	13	AF549051	AF549051 Unculture	c 204	16	80.0	212786	10	AC132395	AC132395 Mus muscu
c 132	16.4	82.0	854	1	UBA440484	UBA440484 Unculture	c 205	16	80.0	216252	2	AC009084	AC009084 Homo sapi
c 133	16.4	82.0	1905	10	AB175682	AB175682 Mus muscu	c 206	16	80.0	218261	2	AC118795	AC118795 Rattus no
c 134	16.4	82.0	2382	1	PSENADHS	M80653 Pseudomonas	c 207	16	80.0	220245	2	AC098122	AC098122 Rattus no
c 135	16.4	82.0	60892	10	AL672130	AL672130 Mouse DNA	c 208	16	80.0	220801	10	AC124604	AC124604 Mus muscu
c 136	16.4	82.0	64120	9	AL445646	AL445646 Human DNA	c 209	16	80.0	222338	2	AC131610	AC131610 Rattus no
c 137	16.4	82.0	60768	2	AC069350	AC069350 Homo sapi	c 210	16	80.0	224215	2	AC114068	AC114068 Rattus no
c 138	16.4	82.0	109860	9	AL359087	AL359087 Human DNA	c 211	16	80.0	225264	2	AC106396	AC106396 Rattus no
c 139	16.4	82.0	110000	2	AC095246	Continuation (3 of	c 212	16	80.0	229330	2	AC137057	AC137057 Rattus no
c 140	16.4	82.0	110000	2	AC095246	Continuation (4 of	c 213	16	80.0	229751	10	AC133200	AC133200 Mus muscu
c 141	16.4	82.0	110000	2	LMFLCHR32	Continuation (13 o	c 214	16	80.0	232535	2	AC110702	AC110702 Rattus no
c 142	16.4	82.0	124489	9	HSJ760C5	AL078587 Human DNA	c 215	16	80.0	238070	2	AC134313	AC134313 Rattus no
c 143	16.4	82.0	132933	9	AL137002	AL137002 Human DNA	c 216	16	80.0	240000	2	AC012525	AC012525 Homo sapi
c 144	16.4	82.0	140137	2	AC027611	AC027611 Homo sapi	c 217	16	80.0	242260	2	AC094567	AC094567 Rattus no
c 145	16.4	82.0	145918	9	AC034229	AC034229 Homo sapi	c 218	16	80.0	243122	2	AC137272	AC137272 Rattus no
c 146	16.4	82.0	147605	2	AC141612	AC141612 Homo sapi	c 219	16	80.0	249565	2	AC097125	AC097125 Rattus no
c 147	16.4	82.0	151847	2	AC022792	AC022792 Homo sapi	c 220	16	80.0	255120	2	AC127219	AC127219 Rattus no
c 148	16.4	82.0	153624	9	HS1018K9	AL031726 Human DNA	c 221	16	80.0	256241	2	AC096075	AC096075 Rattus no
c 149	16.4	82.0	157122	2	AC102699	AC102699 Mus muscu	c 222	16	80.0	322690	2	AC116278	AC116278 Rattus no
c 150	16.4	82.0	158153	2	AC111037	AC111037 Mus muscu	c 223	16	80.0	330608	2	AC109561	AC109561 Rattus no
c 151	16.4	82.0	160390	2	AC129676	AC129676 Homo sapi	c 224	16	80.0	330919	2	AC095296	AC095296 Rattus no
c 152	16.4	82.0	164700	2	AC150838	AC150838 Papio anu	c 225	15.8	79.0	372	8	BT004722	BT004722 Arabidops
c 153	16.4	82.0	165378	9	AC129805	AC129805 Homo sapi	c 226	15.8	79.0	486	4	AF245169	AF245169 Ovis arie
c 154	16.4	82.0	173928	2	AC149564	AC149564 Papio anu	c 227	15.8	79.0	501	1	AY456743	AY456743 Unculture
c 155	16.4	82.0	193528	10	AL772234	AL772234 Mouse DNA	c 228	15.8	79.0	503	1	AY456736	AY456736 Unculture
c 156	16.4	82.0	197637	9	AC023141	AC023141 Homo sapi	c 229	15.8	79.0	503	1	AY457667	AY457667 Unculture
c 157	16.4	82.0	207614	2	AC099800	AC099800 Homo sapi	c 230	15.8	79.0	506	1	AY457666	AY457666 Unculture
c 158	16.4	82.0	209976	2	CR762401	CR762401 Mus muscu	c 231	15.8	79.0	545	8	AK117853	AK117853 Arabidops
c 159	16.4	82.0	219566	2	AC102664	AC102664 Mus muscu	c 232	15.8	79.0	846	5	AY251295	AY251295 Bufo bank
c 160	16.4	82.0	222026	2	AC140449	AC140449 Mus muscu	c 233	15.8	79.0	1074	10	AY029163	AY029163 Rattus no
c 161	16.4	82.0	229533	2	AC106382	AC106382 Rattus no	c 234	15.8	79.0	1372	5	CR406449	CR406449 Gallus ga
c 162	16.4	82.0	245174	2	AC095157	AC095157 Rattus no	c 235	15.8	79.0	1944	6	CQ591783	CQ591783 Sequence
c 163	16.4	82.0	246362	2	AC137868	AC137868 Mus muscu	c 236	15.8	79.0	1965	1	RPHSGEN	Y09979 R.palustris
c 164	16.4	82.0	251084	2	AC120665	AC120665 Rattus no	c 237	15.8	79.0	2072	3	AY058594	AY058594 Drosophil
c 165	16.4	82.0	251932	2	AC137952	AC137952 Mus muscu	c 238	15.8	79.0	2224	5	AJ720284	AJ720284 Gallus ga

c 239	15.8	79.0	2687	6	CQ591788	Sequence	CQ591788	312	15.8	79.0	159408	2	AC141701	AC141701 Apis mell
c 240	15.8	79.0	2702	5	AJ719630	Gallus ga	AJ719630	313	15.8	79.0	159666	2	AC053492	AC053492 Homo sapi
c 241	15.8	79.0	2737	5	BC067919	Xenopus t	BC067919	c 314	15.8	79.0	160008	2	AC022823	AC022823 Homo sapi
c 242	15.8	79.0	2743	5	AY573379	Xenopus l	AY573379	315	15.8	79.0	160527	2	AC145007	AC145007 Bos tauru
c 243	15.8	79.0	2838	1	SAUI19858	Streptomyces	SAUI19858	316	15.8	79.0	160754	9	AC006213	AC006213 Homo sapi
c 244	15.8	79.0	3999	6	CQ591782	Sequence	CQ591782	317	15.8	79.0	161173	10	AC114657	AC114657 Mus muscu
c 245	15.8	79.0	9976	1	AF323755	Rhodococc	AF323755	318	15.8	79.0	162691	2	CNS01DXA	AL139193 Human chr
c 246	15.8	79.0	10029	1	AE012919	Chlorobiu	AE012919	c 319	15.8	79.0	162851	2	AC009637	AC009637 Homo sapi
c 247	15.8	79.0	12382	9	AF207069	Homo sapi	AF207069	c 320	15.8	79.0	163011	10	AC120413	AC120413 Mus muscu
c 248	15.8	79.0	14594	1	AF009826	Pyrobacul	AF009826	c 321	15.8	79.0	164076	2	AC069429	AC069429 Homo sapi
c 249	15.8	79.0	22234	9	AF057159	Homo sapi	AF057159	c 322	15.8	79.0	164911	8	OSJN00209	AL663008 Oryza sat
c 250	15.8	79.0	26073	8	AY534122	Aegilops	AY534122	c 323	15.8	79.0	165358	2	AC009020	AC009020 Homo sapi
c 251	15.8	79.0	34503	2	AC151612	Emiliania	AC151612	c 324	15.8	79.0	165937	8	AC124986	AC124986 Mus muscu
c 252	15.8	79.0	34914	2	AC102932	Mus muscu	AC102932	c 325	15.8	79.0	166474	8	AC083944	AC083944 Genomic s
c 253	15.8	79.0	37752	9	HS361H4C	Human DNA s	HS361H4C	c 326	15.8	79.0	166892	9	AC007463	AC007463 Homo sapi
c 254	15.8	79.0	40571	1	MSGDNAB	Mycobacteri	L39923	c 327	15.8	79.0	168274	2	AL954859	AL954859 Homo sapi
c 255	15.8	79.0	40665	9	HS62D4	Human DNA	AL049747	c 328	15.8	79.0	168317	2	AC048329	AC048329 Homo sapi
c 256	15.8	79.0	40991	1	AY057845	Zymomonas	AY057845	c 329	15.8	79.0	168794	8	AC008726	AC008726 Chlamydom
c 257	15.8	79.0	40996	9	HS4296302	Homo sapi	AJ296302	c 330	15.8	79.0	170021	8	AP003256	AP003256 Oryza sat
c 258	15.8	79.0	42415	9	AC001644	Genomic s	AC001644	c 331	15.8	79.0	171595	9	AC012337	AC012337 Homo sapi
c 259	15.8	79.0	43878	9	BX284655	Human DNA	BX284655	c 332	15.8	79.0	173191	9	AL596114	AL596114 Human DNA
c 260	15.8	79.0	44762	9	AC002325	Homo sapi	AC002325	c 333	15.8	79.0	173877	9	AC108671	AC108671 Homo sapi
c 261	15.8	79.0	46621	9	AL357131	Human DNA	AL357131	c 334	15.8	79.0	174311	3	AC004758	AC004758 Drosophil
c 262	15.8	79.0	48498	8	AC091776	Chlamydom	AC091776	c 335	15.8	79.0	174832	3	AC0092216	AC0092216 Drosophil
c 263	15.8	79.0	53135	9	AC104792	Homo sapi	AC104792	c 336	15.8	79.0	175496	2	AC147330	AC147330 Pan trogl
c 264	15.8	79.0	53335	9	AL593848	Human DNA	AL593848	c 337	15.8	79.0	176425	2	AC090418	AC090418 Homo sapi
c 265	15.8	79.0	64219	5	TRU459419	Takifugu	AJ459419	c 338	15.8	79.0	179756	2	AC074039	AC074039 Mus muscu
c 266	15.8	79.0	78379	2	AC139566	Homo sapi	AC139566	c 339	15.8	79.0	179798	5	BX284110	BX284110 Zebrafish
c 267	15.8	79.0	82098	9	AC006252	Homo sapi	AC006252	c 340	15.8	79.0	179854	2	AC149454	AC149454 Papio anu
c 268	15.8	79.0	87180	8	AB023044	Arabidops	AB023044	c 341	15.8	79.0	180835	9	AC009131	AC009131 Homo sapi
c 269	15.8	79.0	87187	9	AL161744	Human DNA	AL161744	c 342	15.8	79.0	181463	10	AC122452	AC122452 Mus muscu
c 270	15.8	79.0	87947	9	AC137486	Homo sapi	AC137486	c 343	15.8	79.0	181886	9	AC093909	AC093909 Homo sapi
c 271	15.8	79.0	90141	9	AC035150	Homo sapi	AC035150	c 344	15.8	79.0	181921	2	AC091399	AC091399 Bos tauru
c 272	15.8	79.0	98914	2	AC114724	Continuation (4 of	Continuation (15 of	c 345	15.8	79.0	182847	2	AC148229	AC148229 Gallus ga
c 273	15.8	79.0	103566	9	AC003087	Homo sapi	AC003087	c 346	15.8	79.0	183376	2	AC129621	AC129621 Rattus no
c 274	15.8	79.0	103710	9	HSB46817	Human DNA	AC050402	c 347	15.8	79.0	184557	2	AC149554	AC149554 Papio anu
c 275	15.8	79.0	110000	1	EX950851	Erwinia c	EX950851	c 348	15.8	79.0	184835	2	AC068091	AC068091 Homo sapi
c 276	15.8	79.0	110000	2	AP006499	Continuation (2 of	Continuation (15 of	c 349	15.8	79.0	186301	2	AC117735	AC117735 Mus muscu
c 277	15.8	79.0	110000	2	LMFLCHR34_14	Continuation (15 of	Continuation (15 of	c 350	15.8	79.0	187294	2	CR735107	CR735107 Danio rer
c 278	15.8	79.0	111951	9	AC010169	Homo sapi	AC010169	c 351	15.8	79.0	187879	2	AC118479	AC118479 Mus muscu
c 279	15.8	79.0	115483	9	AC108079	Homo sapi	AC108079	c 352	15.8	79.0	188646	2	AC141652	AC141652 Rattus no
c 280	15.8	79.0	118404	4	AL773591	Pig DNA s	AL773591	c 353	15.8	79.0	189983	10	AL928542	AL928542 Mouse DNA
c 281	15.8	79.0	122538	10	AL844557	Mouse DNA	AL844557	c 354	15.8	79.0	191041	2	AC024114	AC024114 Mus muscu
c 282	15.8	79.0	124266	8	AC105744	Oryza sat	AC105744	c 355	15.8	79.0	192131	2	CR392010	CR392010 Danio rer
c 283	15.8	79.0	126462	9	AC004876	Homo sapi	AC004876	c 356	15.8	79.0	192372	2	AC134754	AC134754 Rattus no
c 284	15.8	79.0	129109	9	AL390239	Human DNA	AL390239	c 357	15.8	79.0	192499	2	AC133913	AC133913 Homo sapi
c 285	15.8	79.0	130979	9	AL390719	Human DNA	AL390719	c 358	15.8	79.0	194442	2	AC147724	AC147724 Ocolemur
c 286	15.8	79.0	131042	10	AC110166	Mus muscu	AC110166	c 359	15.8	79.0	194742	9	AC092047	AC092047 Homo sapi
c 287	15.8	79.0	132353	2	AC002335	Homo sapi	AC002335	c 360	15.8	79.0	197552	10	AL606933	AL606933 Mouse DNA
c 288	15.8	79.0	135750	10	AL928859	Mouse DNA	AL928859	c 361	15.8	79.0	198295	2	AC132739	AC132739 Rattus no
c 289	15.8	79.0	138383	8	OSJN00266	Oryza sat	AL731624	c 362	15.8	79.0	198649	8	AY534123	AY534123 Aegilops
c 290	15.8	79.0	139280	9	AC099052	Homo sapi	AC099052	c 363	15.8	79.0	201369	2	AC112993	AC112993 Mus muscu
c 291	15.8	79.0	140488	2	AC017377	Drosophil	AC017377	c 364	15.8	79.0	201748	5	BX000489	BX000489 Zebrafish
c 292	15.8	79.0	140718	9	AL583839	Human DNA	AL583839	c 365	15.8	79.0	202158	5	AL837524	AL837524 Zebrafish
c 293	15.8	79.0	142113	2	AC149745	Bos tauru	AC149745	c 366	15.8	79.0	204165	10	AC124717	AC124717 Mus muscu
c 294	15.8	79.0	142974	2	AC129075	Felis cat	AC129075	c 367	15.8	79.0	204505	9	AC089983	AC089983 Homo sapi
c 295	15.8	79.0	143300	8	AP003630	Oryza sat	AP003630	c 368	15.8	79.0	204795	10	AC123063	AC123063 Mus muscu
c 296	15.8	79.0	143369	9	AC143635	Macaca mu	AC143635	c 369	15.8	79.0	205405	10	AL662893	AL662893 Mouse DNA
c 297	15.8	79.0	144710	2	AC128876	Rattus no	AC128876	c 370	15.8	79.0	206248	10	AC132453	AC132453 Mus muscu
c 298	15.8	79.0	145151	9	AL645949	Human DNA	AL645949	c 371	15.8	79.0	206979	10	AC112683	AC112683 Mus muscu
c 299	15.8	79.0	146376	9	AC009247	Homo sapi	AC009247	c 372	15.8	79.0	209252	9	AC097637	AC097637 Homo sapi
c 300	15.8	79.0	146502	9	AC116456	Homo sapi	AC116456	c 373	15.8	79.0	209480	2	AC140965	AC140965 Pan trogl
c 301	15.8	79.0	146514	2	AC141983	Rattus no	AC141983	c 374	15.8	79.0	212737	2	AC147207	AC147207 Xenopus t
c 302	15.8	79.0	147903	2	AC007681	Homo sapi	AC007681	c 375	15.8	79.0	212940	10	AL591143	AL591143 Mouse DNA
c 303	15.8	79.0	149773	2	AC041029	Homo sapi	AC041029	c 376	15.8	79.0	214160	9	AC094021	AC094021 Homo sapi
c 304	15.8	79.0	150286	2	OSJN00241	Oryza sat	AL731588	c 377	15.8	79.0	214646	2	AC110457	AC110457 Rattus no
c 305	15.8	79.0	150533	9	AL356215	Human DNA	AL356215	c 378	15.8	79.0	215516	2	AC024694	AC024694 Mus muscu
c 306	15.8	79.0	153939	2	AC110906	Mus muscu	AC110906	c 379	15.8	79.0	215516	2	AC024694	AC024694 Mus muscu
c 307	15.8	79.0	154067	2	AC087656	Homo sapi	AC087656	c 380	15.8	79.0	216882	2	AC132716	AC132716 Rattus no
c 308	15.8	79.0	155316	2	AC114646	Mus muscu	AC114646	c 381	15.8	79.0	218427	10	AL772218	AL772218 Mouse DNA
c 309	15.8	79.0	155317	2	AC102022	Mus muscu	AC102022	c 382	15.8	79.0	219200	10	AL589701	AL589701 Mouse DNA
c 310	15.8	79.0	156023	8	AC092173	Oryza sat	AC092173	c 383	15.8	79.0	219280	5	BX004888	BX004888 Zebrafish
c 311	15.8	79.0	158241	8	AP003409	Oryza sat	AP003409	c 384	15.8	79.0	220469	2	AC074307	AC074307 Mus muscu

385	15.8	79.0	220851	5	BX649335	BX649335 Zebrafish	C 458	15.4	77.0	1926	6	BD127163	BD127163 Primer fo
386	15.8	79.0	221307	2	AC094562	AC094562 Rattus no	C 459	15.4	77.0	1926	5	AK074545	AK074545 Homo sapi
C 387	15.8	79.0	221338	5	AC147437	AC147437 Gallus ga	460	15.4	77.0	2025	5	CR761048	CR761048 Xenopus t
C 388	15.8	79.0	223142	2	AC141515	AC141515 Rattus no	C 461	15.4	77.0	2066	5	CR406313	CR406313 Gallus ga
C 389	15.8	79.0	225630	2	AC134035	AC134035 Rattus no	462	15.4	77.0	2068	5	CQ714308	CQ714308 Sequence
C 390	15.8	79.0	226135	2	AC110712	AC110712 Rattus no	463	15.4	77.0	2112	5	BC079696	BC079696 Xenopus l
C 391	15.8	79.0	226164	2	AC127786	AC127786 Rattus no	C 464	15.4	77.0	2132	9	BC042102	BC042102 Homo sapi
C 392	15.8	79.0	226164	2	AC127786	AC127786 Rattus no	C 465	15.4	77.0	2148	6	CQ849559	CQ849559 Sequence
C 393	15.8	79.0	227656	2	AC096253	AC096253 Rattus no	C 466	15.4	77.0	2148	9	AK126577	AK126577 Homo sapi
C 394	15.8	79.0	227656	9	CNS00YVH	AC096869 Human chr	C 467	15.4	77.0	2252	9	BC033499	BC033499 Homo sapi
C 395	15.8	79.0	230191	2	AC148019	AC148019 Mus muscu	468	15.4	77.0	2253	9	UH1866	UH1866 Homo sapien
C 396	15.8	79.0	230879	9	AP003465	AP003465 Homo sapi	469	15.4	77.0	2340	6	CQ741052	CQ741052 Sequence
C 397	15.8	79.0	231537	2	BX677666	BX677666 Danio rer	470	15.4	77.0	2522	6	AX748079	AX748079 Sequence
C 398	15.8	79.0	231811	2	AC120552	AC120552 Mus muscu	471	15.4	77.0	2522	9	AK093365	AK093365 Homo sapi
C 399	15.8	79.0	231811	2	AC094982	AC094982 Rattus no	C 472	15.4	77.0	2522	8	AF348490	AF348490 Neurospor
C 400	15.8	79.0	233762	2	AC094982	AC094982 Rattus no	C 473	15.4	77.0	2866	8	AF348490	AF348490 Neurospor
C 401	15.8	79.0	234885	2	AC097033	AC097033 Rattus no	C 474	15.4	77.0	2923	10	AB096263	AB096263 Mus muscu
C 402	15.8	79.0	236048	2	AC095300	AC095300 Rattus no	C 475	15.4	77.0	2954	3	AF109692	AF109692 Plutella
C 403	15.8	79.0	240155	2	AC135701	AC135701 Rattus no	C 476	15.4	77.0	3049	10	RNSADE	X60822 R.norvegicu
C 404	15.8	79.0	240294	2	AC044892	AC044892 Homo sapi	C 477	15.4	77.0	3058	6	CQ850896	CQ850896 Sequence
C 405	15.8	79.0	241280	2	AC020854	AC020854 Mus muscu	C 478	15.4	77.0	3058	9	AK128093	AK128093 Homo sapi
C 406	15.8	79.0	242705	2	AC027766	AC027766 Mus muscu	C 479	15.4	77.0	3155	3	AY208675	AY208675 Toxoplas
C 407	15.8	79.0	248464	2	AC096438	AC096438 Rattus no	C 480	15.4	77.0	3232	10	MUS8AMSNA	LI3622 Mouse s-ade
C 408	15.8	79.0	252509	2	AC121441	AC121441 Rattus no	481	15.4	77.0	3241	10	BC011211	BC011211 Mus muscu
C 409	15.8	79.0	252833	2	AC130624	AC130624 Rattus no	C 482	15.4	77.0	3245	9	HSPDED3	AF042835 Homo sapi
C 410	15.8	79.0	254217	2	AC114075	AC114075 Rattus no	C 483	15.4	77.0	3284	9	HSTUBB2	X02344 Homo sapien
C 411	15.8	79.0	254538	2	AC097032	AC097032 Rattus no	C 484	15.4	77.0	3361	10	AY350744	AY350744 Mus muscu
C 412	15.8	79.0	256395	2	AC097025	AC097025 Rattus no	C 485	15.4	77.0	3556	10	BC052049	BC052049 Mus muscu
C 413	15.8	79.0	260673	3	AE003612	AE003612 Drosophil	C 486	15.4	77.0	3571	10	BC052722	BC052722 Mus muscu
C 414	15.8	79.0	267672	2	AC093934	AC093934 Rattus no	C 487	15.4	77.0	3582	10	BC048236	BC048236 Mus muscu
C 415	15.8	79.0	268651	2	AX005198	AX005198 Danio rer	C 488	15.4	77.0	3587	10	BC052376	BC052376 Mus muscu
C 416	15.8	79.0	269203	1	MLEPTN130	AL583926 Mycobacte	C 489	15.4	77.0	3832	10	AB099712	AB099712 Mus muscu
C 417	15.8	79.0	270695	10	AC102542	AC102542 Mus muscu	C 490	15.4	77.0	4200	10	AY341261	AY341261 Mus muscu
C 418	15.8	79.0	270808	2	AC102459	AC102459 Mus muscu	C 491	15.4	77.0	4406	5	AJ720105	AJ720105 Gallus ga
C 419	15.8	79.0	274459	2	AC093959	AC093959 Rattus no	C 492	15.4	77.0	4619	10	AK173316	AK173316 Mus muscu
C 420	15.8	79.0	279725	2	AC131174	AC131174 Rattus no	C 493	15.4	77.0	4768	5	CHKTROS04	M21226 Chicken tro
C 421	15.8	79.0	284400	2	AC096840	AC096840 Rattus no	C 494	15.4	77.0	4893	9	AK128726	AK128726 Homo sapi
C 422	15.8	79.0	286283	10	AC139214	AC139214 Mus muscu	C 495	15.4	77.0	6127	6	AX544010	AX544010 Sequence
C 423	15.8	79.0	286358	2	AL713872	AL713872 Mus muscu	C 496	15.4	77.0	6127	9	AF321918	AF321918 Homo sapi
C 424	15.8	79.0	289265	2	AC128986	AC128986 Rattus no	C 497	15.4	77.0	6129	6	CQ573791	CQ573791 Sequence
C 425	15.8	79.0	289265	1	AP005031	AP005031 Streptomy	C 498	15.4	77.0	11259	9	HUMIL8R	M99412 Human inter
C 426	15.8	79.0	300029	8	AE017064	AE017064 Oryza sat	C 499	15.4	77.0	13089	9	AL138970	AL138970 Human DNA
C 427	15.8	79.0	300029	8	AE017066	AE017066 Oryza sat	C 500	15.4	77.0	21092	2	AC014435	AC014435 Drosophil
C 428	15.8	79.0	300550	1	AP005021	AP005021 Streptomy	C 501	15.4	77.0	22186	6	CQ870077	CQ870077 Sequence
C 429	15.8	79.0	308050	1	SCO939124	SCO939124 Streptomy	C 502	15.4	77.0	23704	10	MMQ304861	AJ304861 Mus muscu
C 430	15.8	79.0	327883	2	BX571684	BX571684 Homo sapi	C 503	15.4	77.0	24180	9	AY714242	AY714242 Homo sapi
C 431	15.4	77.0	71	6	AX543989	AX543989 Sequence	C 504	15.4	77.0	25733	9	AP001101	AP001101 Homo sapi
C 432	15.4	77.0	237	9	HS3184R	260687 H.sapiens C	C 505	15.4	77.0	32331	9	BD129574	BD129574 Polynucle
C 433	15.4	77.0	330	11	HS3175VG9	252357 H.sapiens (C 506	15.4	77.0	38186	6	BD129574	BD129574 Polynucle
C 434	15.4	77.0	369	11	GV3842	GV3842 SHGC-84982	C 507	15.4	77.0	38186	9	AC004449	AC004449 Homo sapi
C 435	15.4	77.0	669	11	BV049375	BV049375 S212P6036	C 508	15.4	77.0	43411	9	AC004643	AC004643 Homo sapi
C 436	15.4	77.0	703	9	HS340537	AJ340537 Homo sapi	C 509	15.4	77.0	47950	2	AC099985	AC099985 Mus muscu
C 437	15.4	77.0	773	9	HS340513	AJ340513 Homo sapi	C 510	15.4	77.0	57100	2	AC100002	AC100002 Mus muscu
C 438	15.4	77.0	778	9	HS3439989	AJ3439989 Homo sapi	C 511	15.4	77.0	57901	2	AC004023	AC004023 Homo sapi
C 439	15.4	77.0	782	9	HS3439513	AJ3439513 Homo sapi	C 512	15.4	77.0	61309	2	AC090748	AC090748 Homo sapi
C 440	15.4	77.0	817	1	AB118883	AB118883 Unculture	C 513	15.4	77.0	61672	2	AC133145	AC133145 Homo sapi
C 441	15.4	77.0	817	1	AB118894	AB118894 gamma pro	C 514	15.4	77.0	62172	9	AC140118	AC140118 Homo sapi
C 442	15.4	77.0	873	1	AB136878	AB136878 Unculture	C 515	15.4	77.0	63905	9	AC022515	AC022515 Homo sapi
C 443	15.4	77.0	873	1	AY336881	AY336881 Unculture	C 516	15.4	77.0	70384	9	AC100764	AC100764 Homo sapi
C 444	15.4	77.0	873	1	AY336888	AY336888 Unculture	C 517	15.4	77.0	72508	5	BX248099	BX248099 Zebrafish
C 445	15.4	77.0	873	1	AY336901	AY336901 Unculture	C 518	15.4	77.0	74821	9	AC109642	AC109642 Homo sapi
C 446	15.4	77.0	974	9	HS3438656	AJ3438656 Homo sapi	C 519	15.4	77.0	78647	2	AC100219	AC100219 Mus muscu
C 447	15.4	77.0	1023	5	BC078608	BC078608 Xenopus l	C 520	15.4	77.0	79494	2	AC068837	AC068837 Homo sapi
C 448	15.4	77.0	1176	6	AX598724	AX598724 Sequence	C 521	15.4	77.0	82358	2	AC120872	ContInuatiun (6 of
C 449	15.4	77.0	1185	6	CQ872312	CQ872312 Sequence	C 522	15.4	77.0	85601	9	AC135388	AC092845 Homo sapi
C 450	15.4	77.0	1581	6	AY345341	AY345341 Oryctolag	C 523	15.4	77.0	85801	9	AC093162	AC093162 Homo sapi
C 451	15.4	77.0	1624	10	BC068172	BC068172 Mus muscu	C 524	15.4	77.0	89201	9	AC093162	AC093162 Homo sapi
C 452	15.4	77.0	1636	8	AF127243	AF127243 Nicotiana	C 525	15.4	77.0	91204	2	BX927126	BX927126 Mus muscu
C 453	15.4	77.0	1685	10	BC036332	BC036332 Mus muscu	C 526	15.4	77.0	92205	9	AC007639	AC007639 Homo sapi
C 454	15.4	77.0	1840	6	AX827979	AX827979 Sequence	C 527	15.4	77.0	95291	9	AC124768	AC124768 Homo sapi
C 455	15.4	77.0	1840	6	AX828093	AX828093 Sequence	C 528	15.4	77.0	96595	6	AX695887	AX695887 Sequence
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C 538	15.4	77.0	113367	2	AC149197	AC149197 Medicago
C 539	15.4	77.0	115932	2	AC011446	AC011446 Homo sapi
C 540	15.4	77.0	116205	2	AC148349	AC148349 Medicago
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C 546	15.4	77.0	124112	10	AL645607	AL645607 Mouse DNA
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C 560	15.4	77.0	146443	9	AC007488	AC007488 Homo sapi
C 561	15.4	77.0	146596	9	AC007631	AC007631 Genomic s
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C 581	15.4	77.0	155769	5	AL662861	AL662861 Zebrafish
C 582	15.4	77.0	155960	9	HS288M22	AL662861 Zebrafish
C 583	15.4	77.0	156009	2	AC145001	AC145001 Human DNA
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C 595	15.4	77.0	161970	8	AP003221	AC005137 Human Chr
C 596	15.4	77.0	162777	10	AC121908	AP003221 Oryza sat
C 597	15.4	77.0	164456	10	AC131709	AC121908 Mus muscu
C 598	15.4	77.0	164790	9	AC091108	AC131709 Mus muscu
C 599	15.4	77.0	164815	2	AC013668	AC091108 Homo sapi
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C 621	15.4	77.0	171378	2	AC151303	AC009152 Homo sapi
C 622	15.4	77.0	171394	2	AC023287	AC151303 Xenopus t
C 623	15.4	77.0	171853	9	AP000880	AC023287 Homo sapi
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C 658	15.4	77.0	184695	2	AC145147	AC126553 Mus muscu
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C 665	15.4	77.0	187027	2	AC019078	AC110869 Rattus no
C 666	15.4	77.0	187119	10	AC123533	AC019078 Homo sapi
C 667	15.4	77.0	187587	9	AC016026	AC123533 Mus muscu
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C 673	15.4	77.0	188318	2	CR382343	AC150856 Bos tauru
C 674	15.4	77.0	188779	9	AC090701	CR382343 Danio rer
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RESULT 3
LOCUS       AR365528
DEFINITION  Sequence 3 from patent US 5506344.
ACCESSION  AR365528
VERSION    AR365528.1 GI:34429295
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 623)
AUTHORS   Teujimoto, Y. and Croce, C.A.
TITLE     Antibodies specific for BCL-2 gene product
JOURNAL   Patent: US 5506344-A 3 09-APR-1996;
          Location/Qualifiers
FEATURES   source
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ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 623;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGAGGCGUGGAGGCCUU 20
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Db 477 AACGAGGCTGGGATGCCCTT 496

RESULT 4
LOCUS       AX525911
DEFINITION  Sequence 433 from Patent WO02056682.
ACCESSION  AX525911
VERSION    AX525911.1 GI:25170789
KEYWORDS   Rattus norvegicus (Norway rat)
SOURCE     Rattus norvegicus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE  1
AUTHORS   Farris, G., Hicken, S.H. and Farr, S.B.
TITLE     Rat toxicologically relevant genes and uses thereof
JOURNAL   Patent: WO 02066682-A 433 29-AUG-2002;
          Phase-1 Molecular Toxicology Inc. (US)
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 661;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGAGGCGUGGAGGCCUU 20
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Db 494 AACGAGGCTGGGATGCCCTT 513

RESULT 5
LOCUS       AB116145
DEFINITION  Canis familiaris mRNA for Bcl-2, partial cds.
ACCESSION  AB116145
VERSION    AB116145.1 GI:33411395
KEYWORDS   Canis familiaris (dog)
SOURCE     Canis familiaris
ORGANISM   Canis familiaris

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REFERENCE  1
AUTHORS   Sano, J., Yamazaki, J., Kano, R. and Hasegawa, A.
TITLE     Molecular cloning of canine Bcl-2 family
JOURNAL   Published Only in Database (2003)
REFERENCE  2 (bases 1 to 686)
AUTHORS   Sano, J.
TITLE     Direct Submission
JOURNAL   Submitted (31-JUL-2003) Junichi Sano, Nihon University School of
          Veterinary Medicine, Department of Pathobiology; 1866 Kameino,
          Fujisawa, Kanagawa 252-8510, Japan (E-mail: YRA04720nifty.ne.jp,
          Tel:81-466-84-3649, Fax:81-466-84-3649)
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 20; DB 4; Length 686;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGAGGCGUGGAGGCCUU 20
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Db 318 AACGAGGCTGGGATGCCCTT 337

RESULT 6
LOCUS       RNU34964
DEFINITION  Rattus norvegicus repressor of programmed cell death BCL-2 mRNA,
          complete cds.
ACCESSION  U34964
VERSION    U34964.1 GI:1004378
KEYWORDS   Rattus norvegicus (Norway rat)
SOURCE     Rattus norvegicus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE  1 (bases 1 to 708)
AUTHORS   Tilly, J.L., Tilly, K.I., Kenton, M.L. and Johnson, A.L.
TITLE     Expression of members of the bcl-2 gene family in the immature rat
          ovary: equine chorionic gonadotropin-mediated inhibition of
          granulosa cell apoptosis is associated with decreased bax and
          constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels
          Endocrinology 136 (1), 232-241 (1995)
JOURNAL   MEDLINE
MEDLINE    95129487
PUBMED     7828536
REFERENCE  2 (bases 1 to 708)
AUTHORS   Tilly, J.L., Tilly, K.I., Kenton, M.L. and Johnson, A.L.
TITLE     Direct Submission
JOURNAL   Submitted (28-AUG-1995) Jonathan L. Tilly, Department of Obstetrics
          and Gynecology/Vincent Center for Reproductive Biology,
          Massachusetts General Hospital/Harvard Medical School, 32 Fruit
          Street, Boston, MA 02114, USA
FEATURES   Location/Qualifiers
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CDS

ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 708;
 Best Local Similarity 80.0%; Pred. No. 32;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AACGAGGCGUGGAGCCUU 20
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 Db 565 AACGAGGCTGGGATGCCTT 584

RESULT 7

LOCUS AY509563 711 bp mRNA linear MAM 19-JAN-2004
 DEFINITION Canis familiaris Bcl-2 mRNA, complete cds.
 ACCESSION AY509563
 VERSION AY509563.1 GI:40846416
 KEYWORDS Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 711)
 Chien,M.B., London,C.A. and Jones,C.S.
 Direct Submission
 Submitted (19-DEC-2003) Surgery and Radiology, UC Davis, 2112
 Tupper Hall, One Shields Ave, Davis, CA 95616, USA
 FEATURES Location/Qualifiers
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CDS

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ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 711;
 Best Local Similarity 80.0%; Pred. No. 32;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AACGAGGCGUGGAGCCUU 20
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 Db 565 AACGAGGCTGGGATGCCTT 584

RESULT 8

LOCUS AR487796 711 bp mRNA linear ROD 02-JUN-2003
 DEFINITION Rattus norvegicus Bcl2-like protein mRNA, complete cds.
 ACCESSION AF512835
 VERSION AF512835.1 GI:31324053
 KEYWORDS Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 711)
 Tanaka,T. and Nangaku,M.

LOCUS AR487796 711 bp DNA linear PAT 14-MAY-2004
 DEFINITION Sequence 1 from patent US 6706867.
 ACCESSION AR487796
 VERSION AR487796.1 GI:47253411
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 711)
 AUTHORS Lorenz,M.
 TITLE DNA array sequence selection
 JOURNAL Patent: US 6706867-A 1 16-MAR-2004;
 FEATURES Location/Qualifiers
 source 1..711
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Query Match 100.0%; Score 20; DB 6; Length 711;
 Best Local Similarity 80.0%; Pred. No. 32;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AACGAGGCGUGGAGCCUU 20
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 Db 565 AACGAGGCTGGGATGCCTT 584

RESULT 9

LOCUS AX708370 711 bp DNA linear PAT 04-APR-2003
 DEFINITION Sequence 1 from Patent WO02061135.
 ACCESSION AX708370
 VERSION AX708370.1 GI:29564257
 KEYWORDS Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 711)
 Lorenz,M.
 DNA array sequence selection
 Patent: WO 02061135-A 1 08-AUG-2002;
 THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
 FEATURES Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:10090"

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 Qy 1 AACGAGGCGUGGAGCCUU 20
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 Db 565 AACGAGGCTGGGATGCCTT 584

RESULT 10

LOCUS AF512835 711 bp mRNA linear ROD 02-JUN-2003
 DEFINITION Rattus norvegicus Bcl2-like protein mRNA, complete cds.
 ACCESSION AF512835
 VERSION AF512835.1 GI:31324053
 KEYWORDS Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 711)
 Tanaka,T. and Nangaku,M.

TITLE Rat Bcl2-like protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 711)
AUTHORS Tanaka, T. and Nangaku, M.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Division of Nephrology and Endocrinology, University of Tokyo, 7-3-1 Hongo Bunkyo-ku, Tokyo 113-0033, Japan
FEATURES Location/Qualifiers
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 /db_xref="taxon:10116"
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 /db_xref="GI:31324054"
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 RAYRDPFAMSSQLHLTPFARGRFATVVBELFRDGVNNGRIVAFEPFEGVYMCVSVN
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 Query Match 100.0%; Score 20; DB 10; Length 711;
 Best Local Similarity 80.0%; Pred. No. 32;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTUGGAGGCCUU 20
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Db 565 AACGGAGGCTGGGATGCCTT 584

RESULT 11
LOCUS AR052622 717 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 20 from patent US 5831066.
ACCESSION AR052622
VERSION AR052622.1 GI:5975986
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 717)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 20 03-NOV-1998;
FEATURES Location/Qualifiers
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 /organism="unknown"
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Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 12
LOCUS BD187535 717 bp DNA linear PAT 17-JUL-2003
DEFINITION REGULATION OF bcl-2 GENE EXPRESSION.
ACCESSION BD187535
VERSION BD187535.1 GI:32997274
KEYWORDS JP 2003026609-A/20.
SOURCE unidentified

ORGANISM unidentified
 unclassified.
 1 (bases 1 to 717)
REFERENCE 1 (bases 1 to 717)
AUTHORS Reed, J.C.
TITLE REGULATION OF bcl-2 GENE EXPRESSION
JOURNAL Patent: JP 2003026609-A 20 29-JAN-2003;
COMMENT John C REED
 OS Homo sapiens
 PN JP 2003026609-A/20
 PD 29-JAN-2003
 PP 19-JUN-2002 JP 2002178753
 PR 20-SEP-1993 US 08/124256
 PI John C reed
 CC
FEATURES Key Location/Qualifiers
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Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 13
LOCUS CQ881810 720 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 7 from Patent WO2004083240.
ACCESSION CQ881810
VERSION CQ881810.1 GI:54034589
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Milner, J.
TITLE Regulation of gene expression
JOURNAL Patent: WO 2004083240-A 7 30-SEP-2004;
FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
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QY 1 AACGGAGGCTUGGAGGCCUU 20
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Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 14
LOCUS E49812 720 bp DNA linear PAT 27-AUG-2002
DEFINITION apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
 it, and composition containing the same.
ACCESSION E49812
VERSION E49812.1 GI:22554850
KEYWORDS JP 2001161372-A/1.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 720)
AUTHORS Sibazaki,H. and Kuma,H.
TITLE apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same
JOURNAL Patent: JP 2001161372-A 1 19-JUN-2001;
HISAMITSU PHARMACEUT CO INC
COMMENT OS Homo sapiens (human)
PN JP 2001161372-A/1
PD 19-JUN-2001
PF 09-DEC-1999 JP 1999350427
PI HIROSHI SIBAZAKI,HIDEKAZU KUMA
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P21/04,A61P25/00,
A61P25/28,
PC A61P27/02,A61P43/00,C07K14/47,C12N7/00,C12N15/00,A61K37/02 CC
PC A61P27/02,A61P43/00,C07K14/47,C12N7/00,C12N15/00,A61K37/02 CC
FH Key Location/Qualifiers
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/db_xref="taxon:9606"
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Query Match 100.0%; Score 20; DB 6; Length 720;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AACGAGGCTGGGATGCCTT 593
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Db 574 AACGAGGCTGGGATGCCTT 593

RESULT 15
E49813
LOCUS 720 bp DNA linear PAT 27-AUG-2002
DEFINITION apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same.
ACCESSION E49813
VERSION E49813.1 GI:22554851
KEYWORDS JP 2001161372-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 720)
AUTHORS Sibazaki,H. and Kuma,H.
TITLE apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same
JOURNAL Patent: JP 2001161372-A 2 19-JUN-2001;
HISAMITSU PHARMACEUT CO INC
COMMENT OS Artificial Sequence
PN JP 2001161372-A/2
PD 19-JUN-2001
PF 09-DEC-1999 JP 1999350427
PI HIROSHI SIBAZAKI,HIDEKAZU KUMA
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P21/04,A61P25/00,
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PC A61P27/02,A61P43/00,C07K14/47,C12N7/00,C12N15/00,A61K37/02 CC
PC A61P27/02,A61P43/00,C07K14/47,C12N7/00,C12N15/00,A61K37/02 CC
FH Key Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
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Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Db 574 AACGAGGCTGGGATGCCTT 593

RESULT 16
E49814
LOCUS 720 bp DNA linear PAT 27-AUG-2002
DEFINITION apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same.
ACCESSION E49814
VERSION E49814.1 GI:22554852
KEYWORDS JP 2001161372-A/3.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 720)
AUTHORS Sibazaki,H. and Kuma,H.
TITLE apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same
JOURNAL Patent: JP 2001161372-A 3 19-JUN-2001;
HISAMITSU PHARMACEUT CO INC
COMMENT OS Artificial Sequence
PN JP 2001161372-A/3
PD 19-JUN-2001
PF 09-DEC-1999 JP 1999350427
PI HIROSHI SIBAZAKI,HIDEKAZU KUMA
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P21/04,A61P25/00,
A61P25/28,
PC A61P27/02,A61P43/00,C07K14/47,C12N7/00,C12N15/00,A61K37/02 CC
PC A61P27/02,A61P43/00,C07K14/47,C12N7/00,C12N15/00,A61K37/02 CC
FH Key Location/Qualifiers
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Best Local Similarity 80.0%; Pred. No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Db 574 AACGAGGCTGGGATGCCTT 593

RESULT 17
E49815
LOCUS 720 bp DNA linear PAT 27-AUG-2002
DEFINITION apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same.
ACCESSION E49815
VERSION E49815.1 GI:22554853
KEYWORDS JP 2001161372-A/4.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 720)
AUTHORS Sibazaki,H. and Kuma,H.
TITLE apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same
JOURNAL Patent: JP 2001161372-A 4 19-JUN-2001;
HISAMITSU PHARMACEUT CO INC
COMMENT OS Artificial Sequence
PN JP 2001161372-A/4
PD 19-JUN-2001
PF 09-DEC-1999 JP 1999350427
PI HIROSHI SIBAZAKI,HIDEKAZU KUMA
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P21/04,A61P25/00,
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PC A61P27/02,A61P43/00,C07K14/47,C12N7/00,C12N15/00,A61K37/02 CC
PC A61P27/02,A61P43/00,C07K14/47,C12N7/00,C12N15/00,A61K37/02 CC
FH Key Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 80.0%; Pred. No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Db 574 AACGAGGCTGGGATGCCTT 593

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Db 574 AACGAGGCTGGGATGCCTT 593

RESULT 16
E49814
LOCUS 720 bp DNA linear PAT 27-AUG-2002
DEFINITION apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same.
ACCESSION E49814
VERSION E49814.1 GI:22554852
KEYWORDS JP 2001161372-A/3.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 720)
AUTHORS Sibazaki,H. and Kuma,H.
TITLE apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same
JOURNAL Patent: JP 2001161372-A 3 19-JUN-2001;
HISAMITSU PHARMACEUT CO INC
COMMENT OS Artificial Sequence
PN JP 2001161372-A/3
PD 19-JUN-2001
PF 09-DEC-1999 JP 1999350427
PI HIROSHI SIBAZAKI,HIDEKAZU KUMA
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A61P25/28,
PC A61P27/02,A61P43/00,C07K14/47,C12N7/00,C12N15/00,A61K37/02 CC
PC A61P27/02,A61P43/00,C07K14/47,C12N7/00,C12N15/00,A61K37/02 CC
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Best Local Similarity 80.0%; Pred. No. 32;
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Db 574 AACGAGGCTGGGATGCCTT 593

RESULT 17
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LOCUS 720 bp DNA linear PAT 27-AUG-2002
DEFINITION apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same.
ACCESSION E49815
VERSION E49815.1 GI:22554853
KEYWORDS JP 2001161372-A/4.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 720)
AUTHORS Sibazaki,H. and Kuma,H.
TITLE apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same
JOURNAL Patent: JP 2001161372-A 4 19-JUN-2001;
HISAMITSU PHARMACEUT CO INC
COMMENT OS Artificial Sequence
PN JP 2001161372-A/4
PD 19-JUN-2001
PF 09-DEC-1999 JP 1999350427
PI HIROSHI SIBAZAKI,HIDEKAZU KUMA
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P21/04,A61P25/00,
A61P25/28,
PC A61P27/02,A61P43/00,C07K14/47,C12N7/00,C12N15/00,A61K37/02 CC
PC A61P27/02,A61P43/00,C07K14/47,C12N7/00,C12N15/00,A61K37/02 CC
FH Key Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 80.0%; Pred. No. 32;
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Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 21
BD094979 720 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Apoptosis-inhibiting polypeptides, genes and polynucleotides
ACCESSION BD094979
VERSION WO 0142459-A/3.
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM 1. .720
REFERENCE /organism="synthetic construct"
AUTHORS /mol_type="genomic DNA"
TITLE /db_xref="taxon:32630"
JOURNAL
COMMENT OS Artificial Sequence
PN WO 0142459-A/3
PD 14-JUN-2001
PF 07-DEC-2000 WO 2000JP008667
PR 09-DEC-1999 JP 99P 350427
PI FUTOSHI SHIBAZAKI,HIDEKAZU KUMA
PC C12N15/12,C07K14/82,C12N15/18,A61K38/17,A61K31/711,A61K48/00,
PC A61P43/00,
PC A61P25/28,A61P21/04,A61P9/10,A61P1/16,A61P27/02 CC
Apoptosis-inhibiting polypeptides, genes and polynucleotides CC

CC same, and compositions containing them
FH Key Location/Qualifiers
FT source 1. .720
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Best Local Similarity 80.0%; Pred.No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20
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Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 22
BD094980 720 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Apoptosis-inhibiting polypeptides, genes and polynucleotides
ACCESSION BD094980
VERSION WO 0142459-A/4.
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM 1. (bases 1 to 720)
REFERENCE /organism="synthetic construct"
AUTHORS /mol_type="genomic DNA"
TITLE /db_xref="taxon:32630"
JOURNAL
COMMENT OS Artificial Sequence
PN WO 0142459-A/4
PD 14-JUN-2001
PF 07-DEC-2000 WO 2000JP008667
PR 09-DEC-1999 JP 99P 350427
PI FUTOSHI SHIBAZAKI,HIDEKAZU KUMA
PC C12N15/12,C07K14/82,C12N15/18,A61K38/17,A61K31/711,A61K48/00,
PC A61P43/00,
PC A61P25/28,A61P21/04,A61P9/10,A61P1/16,A61P27/02 CC
Apoptosis-inhibiting polypeptides, genes and polynucleotides CC

CC same, and compositions containing them
FH Key Location/Qualifiers
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Best Local Similarity 80.0%; Pred.No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 23
BD094981 720 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Apoptosis-inhibiting polypeptides, genes and polynucleotides
ACCESSION BD094981
VERSION WO 0142459-A/5.
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM 1. (bases 1 to 720)
REFERENCE /organism="synthetic construct"
AUTHORS /mol_type="genomic DNA"
TITLE /db_xref="taxon:32630"
JOURNAL
COMMENT OS Artificial Sequence
PN WO 0142459-A/5
PD 14-JUN-2001
PF 07-DEC-2000 WO 2000JP008667
PR 09-DEC-1999 JP 99P 350427
PI FUTOSHI SHIBAZAKI,HIDEKAZU KUMA
PC C12N15/12,C07K14/82,C12N15/18,A61K38/17,A61K31/711,A61K48/00,
PC A61P43/00,
PC A61P25/28,A61P21/04,A61P9/10,A61P1/16,A61P27/02 CC
Apoptosis-inhibiting polypeptides, genes and polynucleotides CC

CC same, and compositions containing them
FH Key Location/Qualifiers
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Best Local Similarity 80.0%; Pred.No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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PN WO 0142459-A/4
PD 14-JUN-2001
PF 07-DEC-2000 WO 2000JP008667
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PI FUTOSHI SHIBAZAKI,HIDEKAZU KUMA
PC C12N15/12,C07K14/82,C12N15/18,A61K38/17,A61K31/711,A61K48/00,
PC A61P43/00,
PC A61P25/28,A61P21/04,A61P9/10,A61P1/16,A61P27/02 CC
Apoptosis-inhibiting polypeptides, genes and polynucleotides CC

CC same, and compositions containing them
FH Key Location/Qualifiers
FT source 1. .720
FEATURES
source
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 720;
Best Local Similarity 80.0%; Pred.No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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RESULT 23
BD094981 720 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Apoptosis-inhibiting polypeptides, genes and polynucleotides
ACCESSION BD094981
VERSION WO 0142459-A/5.
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM 1. (bases 1 to 720)
REFERENCE /organism="synthetic construct"
AUTHORS /mol_type="genomic DNA"
TITLE /db_xref="taxon:32630"
JOURNAL
COMMENT OS Artificial Sequence
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PD 14-JUN-2001
PF 07-DEC-2000 WO 2000JP008667
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PI FUTOSHI SHIBAZAKI,HIDEKAZU KUMA
PC C12N15/12,C07K14/82,C12N15/18,A61K38/17,A61K31/711,A61K48/00,
PC A61P43/00,
PC A61P25/28,A61P21/04,A61P9/10,A61P1/16,A61P27/02 CC
Apoptosis-inhibiting polypeptides, genes and polynucleotides CC

CC same, and compositions containing them
FH Key Location/Qualifiers
FT source 1. .720
FEATURES
source
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 720;
Best Local Similarity 80.0%; Pred.No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AACGGAGGCGUGGAUGCCUU 20
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Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 24
AR021160
LOCUS AR021160 760 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 11 from patent US 5789389.
ACCESSION AR021160
VERSION AR021160.1 GI:3975775
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 760)
AUTHORS Tarasiewicz D.G., Schott B., Holzmayer T.A. and Roninson I.B.
TITLE BCL2 derived genetic elements associated with sensitivity to chemotherapeutic drugs
JOURNAL Patent: US 5789389-A 11 04-AUG-1998;
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/organism="unknown"
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ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 760;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCGUGGAUGCCUU 20
|||||:||||:||||:
Db 594 AACGGAGGCTGGGATGCCTT 613

RESULT 25
A76121
LOCUS A76121 765 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 1 from Patent WO9320200.
ACCESSION A76121
VERSION A76121.1 GI:6088257
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 765)
AUTHORS Evan G.I.
TITLE MODIFIED CELLS AND METHOD OF TREATMENT
JOURNAL Patent: WO 9320200-A 1 14-OCT-1993;
IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)
FEATURES
source Location/Qualifiers
1. 765
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/chromosome="18"
31. 750
/note="unnamed protein product"
/codon_start=1
/protein_id="CAB58588.1"
/db_xref="GI:6088258"
/translations="MAHAGRTGYDNEIRVMKYIHYKLSORGVEWDAGDVGAAAPGAAP
APGIFSSQGHTPHAPADVPARTSPLQTPAPGAAGPALSPVPVVLALRQAGD
DFSRRYRGDFPAEMSQHLTPFTARGFAIVVEELFRDGVNWRGRIIVAFRFGVMQVE
SVNRESPLDVNLALMTYLNHLHTWTIQDNGGWDFAVELYGPSMRPLDFDLSLX
TLLSLALVGACITLGLSHK"

CDS
Query Match 100.0%; Score 20; DB 6; Length 765;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
ORIGIN

QY 1 AACGGAGGCGUGGAUGCCUU 20
|||||:||||:||||:
Db 604 AACGGAGGCTGGGATGCCTT 623

RESULT 26
E58776
LOCUS E58776 771 bp DNA linear PAT 31-JAN-2002
DEFINITION Screening method of apoptosis inhibitor or promoter.
ACCESSION E58776
VERSION E58776.1 GI:18622308
KEYWORDS JP 2000287689-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 771)
AUTHORS Tsujimoto Y. and Simizu S.
TITLE Screening method of apoptosis inhibitor or promoter
JOURNAL Patent: JP 2000287689-A 1 17-OCT-2000;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2000287689-A/1
PD 17-OCT-2000
PF 08-APR-1999 JP 1999101888
PR YOSHIHIDE TSUJIMOTO, SHIGEOMI SIMIZU
PC C12N15/09, A61K31/00, A61K38/00, A61K45/00, C07K14/47, C07K14/705,
PC C12N5/10,
PC C12P21/02, G01N33/15, G01N33/50, C12N15/00, A61K37/02, C12N5/00 CC

PH Key Location/Qualifiers
FT CDS Location/Qualifiers
1. 771
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 771;
Best Local Similarity 80.0%; Pred. No. 31;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCGUGGAUGCCUU 20
|||||:||||:||||:
Db 605 AACGGAGGCTGGGATGCCTT 624

RESULT 27
E23358
LOCUS E23358 953 bp DNA linear PAT 18-JUN-2001
DEFINITION Virus vector system expressing apoptosis-related gene.
ACCESSION E23358
VERSION E23358.1 GI:13024381
KEYWORDS JP 1999075859-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 953)
AUTHORS Hirofumi H.
TITLE Virus vector system expressing apoptosis-related gene
JOURNAL Patent: JP 1999075859-A 4 23-MAR-1999;
COMMENT R B R JENSERU KK
OS Homo sapiens (human)
PN JP 1999075859-A/4
PD 23-MAR-1999
PF 08-SEP-1997 JP 1997259235
PR HIROFUMI HAMADA
PC C12N15/09, C12N5/10, C12N7/00//A61K35/76, A61K48/00, (C12N5/10, PC
C12R1:91),

AUTHORS Yamazaki, J., Sano, J., Kano, R. and Hasegawa, A.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2002) Rui Kano, Nihon University School of Veterinary Medicine, Department of Pathobiology; Kameino 1866, Fujisawa, Kanagawa 252-8510, Japan (E-mail: Kano@rs.nihon-u.ac.jp, Tel: 81-466-84-3649 (ex. 2128), Fax: 81-466-84-3649)
FEATURES Location/Qualifiers
 source
 1..1423
 /organism="Felis catus"
 /mol_type="mRNA"
 /db_xref="taxon:9685"
 /cell_line="FT-1"
 /cell_type="lymphocyte"
 1..1423
 /genes="bcl-2"
 1..513
 /genes="bcl-2"
 514..1221
 /genes="bcl-2"
 /codon_start=1
 /product="bcl-2 protein"
 /protein_id="BAC24136.1"
 /db_xref="GI:25166611"
 /translation="MAHAGRTGYDNRIVMKYIHYELPQRYEWDAAGAAPGGAAP
 AGIFSSQGRTPAPARTSPPPVAPAAAAAGPALSPVPVHLTLRQAGDDFSR
 RYRDPAEWSSQLHLTPFTARGRFATVVEELFDGYNWGRIVAFEFGGVMCGVNR
 EMSPVLNIALMTEYLNRLHLTWIQDNGGWDAFVELYGPSMQLPFDFFSWSLSLK
 LALVGACITIGAYLGHK"
 1222..1423
 /genes="bcl-2"
 3' UTR
 1222..1423
 /genes="bcl-2"
ORIGIN
Query Match 100.0%; Score 20; DB 4; Length 1423;
Best Local Similarity 80.0%; Pred. No. 29;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGTCUGGAUGCCUU 20
|||||:||||:||||:
Db 1075 AACGGAGGTCGGATCCCTT 1094

RESULT 31
LOCUS AR054009 1846 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5834306.
ACCESSION AR054009
VERSION AR054009.1 GI:5978871
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1846)
AUTHORS Webster, K.A. and Bishopric, N.H.
TITLE Tissue specific hypoxia regulated therapeutic constructs
JOURNAL Patent: US 5834306-A 16 10-NOV-1998;
FEATURES Location/Qualifiers
 source
 1..1846
 /organism="unknown"
 /mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1846;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGTCUGGAUGCCUU 20
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Db 1460 AACGGAGGTCGGATCCCTT 1479

RESULT 32
LOCUS AR146185 1846 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 16 from patent US 6218179.
ACCESSION AR146185
VERSION AR146185.1 GI:15109374
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1846)
AUTHORS Webster, K.A., Bishopric, N.H., Murphy, B., Laderoute, K.R. and Green, C.J.
TITLE Tissue specific hypoxia regulated constructs
JOURNAL Patent: US 6218179-A 16 17-APR-2001;
FEATURES Location/Qualifiers
 source
 1..1846
 /organism="unknown"
 /mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1846;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGTCUGGAUGCCUU 20
|||||:||||:||||:
Db 1460 AACGGAGGTCGGATCCCTT 1479

RESULT 33
LOCUS HSBCL21G 1846 bp mRNA linear PRI 26-MAR-1993
DEFINITION H.sapiens mRNA for bcl2-Ig fusion gene.
ACCESSION X06487
VERSION X06487.1 GI:288447
KEYWORDS bcl2-Ig fusion gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1846)
AUTHORS Seto, M., Jaeger, U., Hockett, R.D., Graninger, W., Bennett, S., Goldman, P. and Korsmeyer, S.J.
TITLE Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-Ig fusion gene in lymphoma
JOURNAL EMBO J. 7 (1), 123-131 (1988)
MEDLINE 88196071
PUBMED 2834197
FEATURES Location/Qualifiers
 source
 1..1846
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 1..1846
 /genes="bcl2-Ig fusion gene"
 887..1806
 /genes="bcl2-Ig fusion gene"
 /codon_start=1
 /protein_id="CAA29778.1"
 /db_xref="GI:288448"
 /db_xref="GOA:P10415"
 /db_xref="UniProt/Swiss-Prot:P10415"
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 APGFSRQDHTPHPAASRDVARTSPQTAPAGAAAGPALSPVPVHLTLRQAGD
 DPSRRYRDFAEMSSQLHLTPFTARGCFATVVEELFDGYNWGRIVAPPEFGVMCGVE
 SVNREMSPLVNIALMTEYLNRLHLTWIQDNGGWDAFVELYGPSMRPLPDPFSWSLSLK
 TLLSLALVGACITIGAYLGHK"
ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 1846;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGTCUGGAUGCCUU 20
|||||:||||:||||:

Db 1460 AACGGAGGCTGGGATGCCTT 1479

RESULT 34
CQ769647

DEFINITION Sequence 373 from Patent WO2003058021.
ACCESSION CQ769647
VERSION CQ769647.1 GI:45114164
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
Koenig-Hoffman, K., Kazinski, M., Schaefer, R. and Kesper, B.
Novel apoptosis-inducing dna sequences
Patent: WO 2003058021-A 373 17-JUL-2003;
Xantos Biomedicine AG (DE)

JOURNAL Xantos Biomedicine AG (DE)

FEATURES
source
1..2704
/location=Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 2704;
Best Local Similarity 80.0%; Pred. No. 26;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGATGCCTT 20
|||||:|||||:|||||:
Db 963 AACGGAGGCTGGGATGCCTT 982

RESULT 35
BC027258

LOCUS Homo sapiens B-cell CLL/lymphoma 2, transcript variant alpha, mRNA
DEFINITION (cDNA clone MGC:21366 IMAGE:4511027), complete cds.
ACCESSION BC027258
VERSION BC027258.1 GI:20072667
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2704)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Hahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
JOURNAL 12477932
PUBMED
REFERENCE 2 (bases 1 to 2704)
AUTHORS Straussberg, R.
TITLE Direct Submission

Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapsb@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAC Plate: 28 Row: h Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557356.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:21366 IMAGE:4511027"
/tissue_type="Testis, embryonal carcinoma"
/clone_lib="NIH MGC_92"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
1..2704
/gene="BCL2"
/notes="synonym: Bcl-2"
/db_xref="LocusID:596"
/db_xref="MIM:151430"
390..1109
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/codon_start=1
/product="B-cell lymphoma protein 2, alpha isoform"
/protein_id="AAH27258.1"
/db_xref="GI:20072668"
/db_xref="LocusID:596"
/db_xref="MIM:151430"
/translation="MAHAGRTGYDNRREIVMKYTHYKLSQRGYEWADGVGAAPGAPAPGIFSSQCHTTPAASRDPPVARTSLQTPAAGAAAGPALSPVPVPHLTTRQAGD DFRRRYRRDPAEMSSQLHLPFTARGRFATVVEELFRDGVNMGRIVAFPEFGVMCVS SVNREMSPLVDNLALNWTENLHRLHTWIQDNGWDFAVELYGPSMRPLPDFSWLSLK TLLSLALVGCITLGYLGHK"

Qy 1 AACGGAGGCTGGGATGCCTT 20
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Db 963 AACGGAGGCTGGGATGCCTT 982

RESULT 36
AR365070

LOCUS AR365070
DEFINITION Sequence 1 from patent US 5459251.
ACCESSION AR365070
VERSION AR365070.1 GI:34428349
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

Query Match 100.0%; Score 20; DB 9; Length 2704;
Best Local Similarity 80.0%; Pred. No. 26;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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REFERENCE 1 (bases 1 to 4825)
AUTHORS Teufelmo, Y. and Croce, C.A.
TITLE DNA molecules having human bcl-2 gene sequences
JOURNAL Patent: US 5459251-A 1 17-OCT-1995;
FEATURES Location/Qualifiers
source 1..4825
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 4825;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCTGGGATGCCTT 2051
Db 2032 AACGGAGGCTGGGATGCCTT 2051
RESULT 37
LOCUS AR052621 5086 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5831066.
ACCESSION AR052621
VERSION AR052621.1 GI:5975985
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5086)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 19 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..5086
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCTGGGATGCCTT 2051
Db 2032 AACGGAGGCTGGGATGCCTT 2051
RESULT 38
LOCUS AR054008 5086 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5834306.
ACCESSION AR054008
VERSION AR054008.1 GI:5978870
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5086)
AUTHORS Webster, K.A. and Bishopric, N.H.
TITLE Tissue specific hypoxia regulated therapeutic constructs
JOURNAL Patent: US 5834306-A 14 10-NOV-1999;
FEATURES Location/Qualifiers
source 1..5086
/organism="unknown"
/mol_type="unassigned DNA"
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Query Match 100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCTGGGATGCCTT 2051
Db 2032 AACGGAGGCTGGGATGCCTT 2051
RESULT 39
LOCUS AR146184 5086 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 14 from patent US 6218179.
ACCESSION AR146184
VERSION AR146184.1 GI:15109373
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5086)
AUTHORS Webster, K.A., Bishopric, N.H., Murphy, B., Laderoute, K.R. and Green, C.J.
TITLE Tissue specific hypoxia regulated constructs
JOURNAL Patent: US 6218179-A 14 17-APR-2001;
FEATURES Location/Qualifiers
source 1..5086
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCTGGGATGCCTT 2051
Db 2032 AACGGAGGCTGGGATGCCTT 2051
RESULT 40
LOCUS BD187534 5086 bp DNA linear PAT 17-JUL-2003
DEFINITION REGULATION OF bcl-2 GENE EXPRESSION.
ACCESSION BD187534
VERSION BD187534.1 GI:32997273
KEYWORDS JP 2003026609-A/19.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 5086)
AUTHORS Reed, J.C.
TITLE REGULATION OF bcl-2 GENE EXPRESSION
JOURNAL Patent: JP 2003026609-A 19 29-JAN-2003;
COMMENT OS Homosapiens
PN JP 2003026609-A/19
PD 29-JAN-2003
PP 19-JUN-2002 JP 2002178753
PR 20-SEP-1993 US 08/124256
PI John C Reed
CC
FH Key Location/Qualifiers.
FEATURES Location/Qualifiers
source 1..5086
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCTGGGATGCCTT 2051
Db 2032 AACGGAGGCTGGGATGCCTT 2051
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RESULT 41
AR237427          5086 bp      DNA      linear      PAT 20-DEC-2002
LOCUS
DEFINITION       Sequence 7 from patent US 6465617.
ACCESSION        AR237427
VERSION          AR237427.1  GI:27282148
KEYWORDS
SOURCE           Unknown.
ORGANISM         Unknown.
REFERENCE        1 (bases 1 to 5086)
AUTHORS         Horvitz,H.R. and Hengartner,M.
TITLE           Identification and characterization of a gene which protects cells
                from programmed cell death and uses therefor
JOURNAL         Patent: US 6465617-A 7 15-OCT-2002;
FEATURES         Location/Qualifiers
source           1..5086
                /organism="unknown"
                /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAGCCUU 20
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Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 42
BD008997
LOCUS
DEFINITION       Inhibition of Bcl-2 protein expression by liposomal antisense
                oligodeoxynucleotides.
ACCESSION        BD008997
VERSION          BD008997.1  GI:18637370
KEYWORDS         JP 2001502172-A/4.
SOURCE           unidentified
ORGANISM         unidentified
REFERENCE        1 (bases 1 to 5086)
AUTHORS         Tormo,M., Tara,A.M., Berestein,G.L. and McDonnell,T.J.
TITLE           Inhibition of Bcl-2 protein expression by liposomal antisense
                oligodeoxynucleotides
JOURNAL         Patent: JP 2001502172-A 4 20-FEB-2001;
                BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM
COMMENT          OS Unidentified
                PN JP 2001502172-A/4
                PD 20-FEB-2001
                PF 03-OCT-1997 JP 1998516985
                PR 04-OCT-1996 US 08/726211
                PI MAR TORMO,ANA M TARA,GABRIEL LOPEZ BERESTEIN, PI TIMOTHY J
                MCDONNELL
                PC A61K9/127,A61K31/70,C07H21/04,C12N15/00
                CC Strandedness: Single;
                CC Topology: Linear;
                FH Key Location/Qualifiers
                FT CDS 1459..2175.

FEATURES         source
                Location/Qualifiers
                1..5086
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ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAGCCUU 20
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Db 2032 AACGGAGGCTGGGATGCCTT 2051
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RESULT 43
BD084821
LOCUS
DEFINITION       Diagnosis method and reagents.
ACCESSION        BD084821
VERSION          BD084821.1  GI:22630431
KEYWORDS         JP 2001522241-A/14.
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE        1 (bases 1 to 5086)
AUTHORS         Leeuwen,F.W.V., Grosveld,F.G. and Burbach,J.P.H.
TITLE           Diagnosis method and reagents
JOURNAL         Patent: JP 2001522241-A 14 13-NOV-2001;
                ROYAL NETHERLANDS ACADEMY OF ARTS AND SCIENCES, ERASMUS UNIVERSITY
                ROTTERDAM, UNIVERSITY OF UTRECHT
COMMENT          OS Homo sapiens (human)
                PN JP 2001522241-A/14
                PD 13-NOV-2001
                PF 02-APR-1998 JP 1998542545
                PR 10-APR-1997 US 60/043163
                PI FREDERIK W VAN LEEUWEN,FRANKLIN G GROSVELD,JOHANNES PETER PI
                HENRI BURBACH
                PC C12Q1/68,C07K14/47,C12N15/52,C12N9/00,C12N5/10,A61K38/43, PC
                A01K67/027,
                CC A01K48/00//C07K16/18
                CC Strandedness: Double;
                CC Topology: Linear;
                CC B-cell leukemia
                CC /lymphoma 2 (bcl-2) protooncogene mRNA, Genbank accession CC
                FH Key Location/Qualifiers
                FT source 1..5086
                /organism="Homo sapiens (human)".

FEATURES         source
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                /mol_type="genomic DNA"
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ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAGCCUU 20
|||||:|||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 44
HUMBCL2A
LOCUS
DEFINITION       Human B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene mRNA
                encoding bcl-2-alpha protein, complete cds.
ACCESSION        M13994
VERSION          M13994.1  GI:179366
KEYWORDS         alternative splicing; bcl-2-alpha protein; proto-oncogene.
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE        1 (bases 1 to 5086)
AUTHORS         Tsujimoto,Y. and Croce,C.M.
TITLE           Analysis of the structure, transcripts, and protein products of
                bcl-2, the gene involved in human follicular lymphoma
JOURNAL         Proc. Natl. Acad. Sci. U.S.A. 83 (14), 5214-5218 (1986)
MEDLINE          86259760
PUBMED           3523487
COMMENT          Original source text: Human pre-B-cell leukemia cell line 380, cDNA
```

to mRNA, clones B[3,4,10]; and DNA, clone lambda-18-27.
Clean copy sequence for [1] kindly provided by Y.Tsuimoto.

The bcl-2 gene is transcribed by alternative splicing into three mRNAs of different sizes. It consists of at least two exons and encodes two proteins which only differ at their carboxy-terminal ends, and it is activated by translocation into proximity with the Ig heavy chain locus. Both the normal and rearranged bcl-2 gene products are expressed in the B-cell leukemia/lymphoma 2 cells. Genomic clone lambda-18-27 contained all the DNA sequences on the 5' of the splice site (position 2044).

```

FEATURES
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            /map="18q21.3"
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    mRNA
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            /codon_start=1
            /protein_id="AAA51813.1"
            /db_xref="GI:179367"
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            /translations="MAHAGRTGYDNEIRVIMKYIHYKLSQRYENDAGDVGAAPPGGAAP
            APGIFSSQSGHTPHPAASRDVPARTPLQTPAAGAAAGPALSFPVPVHLALRQAGD
            DFSRRYRGDFAEWSSQLHPTPTARGFATVVEELPRDGVNMGRIVAFPEFGVMCWE
            SYNREMSPLVDNLAMWTEYLNRHLHTWIQDNGGWDFAVELYGPSMRPLDFSWLSLK
            TLLSLALVGACITLGAYLGHK"
    ORIGIN
        710 bp upstream of Set1 site.

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Query Match      100.0%; Score 20; DB 9; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGATGCCCTT 2051
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Db 2032 AACGGAGGCTGGGATGCCCTT 2051

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RESULT 45
AX277471
LOCUS      AX277471      5087 bp      DNA      linear      PAT 29-OCT-2001
DEFINITION Sequence 11 from Patent WO0160998.
ACCESSION AX277471
VERSION    AX277471.1 GI:16548989
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Tari, A.M., Lopez-Berestein, G. and Gutierrez-Puente, Y.
TITLE      Small oligonucleotides with anti-tumor activity
JOURNAL    Patent: WO 0160998-A 11 23-AUG-2001,
            Board of Regents, The University of Texas System (US)
FEATURES
    source
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
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            /notes="unnamed protein product; Synthetic Primer"
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            /transl_table=11
            /protein_id="CAD10340.1"
            /db_xref="GI:16548990"
            /translations="MAHAGRTGYDNEIRVIMKYIHYKLSQRYENDAGDVGAAPPGGAAP
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FEATURES
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            /translations="MAHAGRTGYDNEIRVIMKYIHYKLSQRYENDAGDVGAAPPGGAAP
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```

DFSRYRGDFAEWSSQLHPTPTARGFATVVEELPRDGVNMGRIVAFPEFGVMCWE
SYNREMSPLVDNLAMWTEYLNRHLHTWIQDNGGWDFAVELYGPSMRPLDFSWLSLK
TLLSLALVGACITLGAYLGHK"

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```

ORIGIN
    Query Match      100.0%; Score 20; DB 6; Length 5087;
    Best Local Similarity 80.0%; Pred. No. 24;
    Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 2032 AACGGAGGCTGGGATGCCCTT 2051

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```

RESULT 46
AR365527
LOCUS      AR365527      5104 bp      DNA      linear      PAT 03-SEP-2003
DEFINITION Sequence 1 from patent US 5506344.
ACCESSION AR365527
VERSION    AR365527.1 GI:34429294
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 5104)
AUTHORS    Tsujimoto, Y. and Croce, C.A.
TITLE      Antibodies specific for BCL-2 gene product
JOURNAL    Patent: US 5506344-A 1 09-APR-1996;
            Location/Qualifiers
FEATURES
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```

ORIGIN
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    Best Local Similarity 80.0%; Pred. No. 24;
    Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 2032 AACGGAGGCTGGGATGCCCTT 2051

```

```

RESULT 47
I08038
LOCUS      I08038      5105 bp      DNA      linear      PAT 02-DEC-1994
DEFINITION Sequence 1 from Patent EP 0252685.
ACCESSION I08038
VERSION    I08038.1 GI:589249
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 5105)
AUTHORS    Tsujimoto, Y. and Croce, C.M.
TITLE      Diagnostic methods for detecting lymphomas in humans
JOURNAL    Patent: EP 0252685-A2 1 13-JAN-1988;
            Location/Qualifiers
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ORIGIN
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    Best Local Similarity 80.0%; Pred. No. 24;
    Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGATGCCCTT 2051
|||||:|||||:|||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCCTT 2051

```

```

RESULT 48

```

Fert. V.
TITLE Gene expression profiling of primary breast carcinomas using arrays
of candidate genes
JOURNAL Patent: WO 0246467-A 117 13-JUN-2002;
Ipsoclen (FR)

FEATURES	source
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Best Local Similarity 80.0%; Pred. NO. 23;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
On 1 AAGCGAGGCGTGGGAGGCGCTTT 20

```

```

Db      605 AACGGAGGCTGGGATGCCTT 624
|||||:||||:||||:||||:
Search completed: May 24, 2005. 05:28:25

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Job time : 1938 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 04:23:02 ; Search time 432 Seconds
(without alignments)
274.062 Million cell updates/sec

Title: us-10-018-437-2

Perfect score: 20
Sequence: 1 aacgagcguggaugccuu 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 750 summaries

Database : N_Genseq_16Dec04:*

- 1: Genseq1990s:*
- 2: Genseq1990s:*
- 3: Genseq2000s:*
- 4: Genseq2001as:*
- 5: Genseq2001bs:*
- 6: Genseq2002as:*
- 7: Genseq2002bs:*
- 8: Genseq2003as:*
- 9: Genseq2003bs:*
- 10: Genseq2003cs:*
- 11: Genseq2003ds:*
- 12: Genseq2004as:*
- 13: Genseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	4	AAC86402
2	20	100.0	20	4	AAC86403
3	20	100.0	599	12	ADO05981
4	20	100.0	660	6	ABT09345
5	20	100.0	661	12	ADH22708
6	20	100.0	661	13	ADR91070
7	20	100.0	711	6	ABQ74483
8	20	100.0	711	11	ACN45149
9	20	100.0	717	6	ABQ74483
10	20	100.0	717	6	ABL54167
11	20	100.0	720	4	AAH45294
12	20	100.0	720	4	AAH45293
13	20	100.0	720	4	AAH45297
14	20	100.0	720	4	AAH45296
15	20	100.0	720	4	AAH45295
16	20	100.0	720	6	ABA92889
17	20	100.0	720	13	ADR28075
18	20	100.0	720	10	ADR46370
19	20	100.0	720	13	ADS74141
20	20	100.0	760	2	AAT33694

21	20	100.0	765	2	AAQ49815	AaQ49815 Bcl-2. 3/
22	20	100.0	771	4	AAC90809	Aac90809 Human Bcl
23	20	100.0	931	12	ADO70418	Ado70418 Human Bcl
24	20	100.0	931	12	ADO70435	Ado70435 Human Bcl
25	20	100.0	953	2	AAx33183	Aax33183 Bcl-2 DNA
26	20	100.0	1179	10	ADB58219	Adb58219 Toxicity-
27	20	100.0	1179	10	ADB52744	Adb52744 Primary r
28	20	100.0	2704	10	ADI62930	Adi62930 Human apo
29	20	100.0	5085	6	ABQ78540	Abq78540 Nucleotid
30	20	100.0	5086	2	AAQ54631	AaQ54631 Human onc
31	20	100.0	5086	2	AAQ86661	AaQ86661 Human bcl
32	20	100.0	5086	2	AAx75766	Aax75766 Human bcl
33	20	100.0	5086	6	ABL54166	AbL54166 DNA seque
34	20	100.0	5086	8	ABV75366	Abv75366 Human Bcl
35	20	100.0	5086	9	ACD28370	AcD28370 cDNA enco
36	20	100.0	5086	12	ADG87140	Adg87140 Human Bcl
37	20	100.0	5087	5	AAD15284	Aad15284 Human Bcl
38	20	100.0	5105	1	AAH81292	Aah81292 Sequence
39	20	100.0	6030	6	ABV94126	Abv94126 Breast ca
40	20	100.0	6030	8	ABT16640	Abt16640 Human bcl
41	20	100.0	6030	10	ADE84951	AdE84951 Farnesyl
42	20	100.0	6030	10	ADG32700	Adg32700 Human DNA
43	20	100.0	6030	10	ADH28919	Adh28919 Human chr
44	20	100.0	6030	10	ADG89341	Adg89341 Cancer de
45	20	100.0	6030	11	ADI31689	Adi31689 Human cDN
46	20	100.0	6030	12	ADL83240	Adl83240 Human PRO
47	20	100.0	6030	12	ADO19395	Ado19395 Human PRO
48	20	100.0	6030	13	ADR24647	Adr24647 Breast ca
49	20	100.0	6032	4	AAC84600	Aac84600 Human BCL
50	20	100.0	6142	11	ACN92553	Acn92553 Breast ca
51	20	100.0	7364	8	ACC46612	Acc46612 Human dit
52	20	100.0	7996	2	AAx33184	Aax33184 Base sequ
53	18.4	92.0	20	4	AAC86405	Aac86405 Human bcl
54	18.2	91.0	29	3	AAC65050	Aac65050 Human bcl
55	17.4	87.0	2779	5	AAH83938	Aah83938 DNA encod
56	16.8	84.0	379	11	ADL31106	AdL31106 Human cDN
57	16.8	84.0	863	12	ACH87700	Ach87700 Human gen
58	16.8	84.0	950	6	ABX710374	Abx710374 Human bon
59	16.8	84.0	1154	8	ABX71106	Abx71106 Novel hum
60	16.8	84.0	2206	4	ABL27709	AbL27709 Drosophil
61	16.8	84.0	3051	10	ADC30123	Adc30123 Human nov
62	16.8	84.0	4206	4	ABU27708	AbU27708 Drosophil
63	16.4	82.0	695	3	AAC81410	Aac81410 Pseudomon
64	16.4	82.0	1147	3	AAC81409	Aac81409 Pseudomon
65	16.4	82.0	2382	3	AAC81406	Aac81406 Pseudomon
66	16.2	81.0	20	3	AAC65051	Aac65051 Human bcl
67	16	80.0	1901	3	AAZ44679	Aaz44679 Rat liver
68	16	80.0	1910	10	ADB57944	AdB57944 Toxicity-
69	16	80.0	1910	10	ADB53450	AdB53450 Primary r
70	15.8	79.0	372	3	AAC54725	Aac54725 Arabidops
71	15.8	79.0	534	3	AAC52649	Aac52649 Arabidops
72	15.8	79.0	543	3	AAC54727	Aac54727 Arabidops
73	15.8	79.0	1332	11	ADM33852	Adm33852 DNA encod
74	15.8	79.0	1332	13	ADR48983	Adr48983 HUEPO-L-F
75	15.8	79.0	1368	11	ADM33375	Adm33375 Human GCS
76	15.8	79.0	1594	6	ABK90208	Abk90208 Human cDN
77	15.8	79.0	1944	4	ABU14867	AbU14867 Drosophil
78	15.8	79.0	2687	4	ABU14870	AbU14870 Drosophil
79	15.8	79.0	3821	8	ACA40009	Aca40009 Prokaryot
80	15.8	79.0	3999	4	ABU14866	AbU14866 Drosophil
81	15.8	79.0	6149	4	AAU07166	Aal07166 Human rep
82	15.8	79.0	8031	4	AAU07167	Aal07167 Human rep
83	15.8	79.0	8066	4	AAU07168	Aal07168 Human rep
84	15.8	79.0	12382	12	AQI19186	Adq19186 Human eof
85	15.8	79.0	30030	11	ACN44714	Acn44714 Human gen
86	15.8	79.0	31898	11	ACN44354	Acn44354 Human gen
87	15.8	79.0	82615	9	ACA60905	AcA60905 Human tra
88	15.8	79.0	98690	6	ABK12169	Abk12169 Human DNA
89	15.4	77.0	71	6	ABS52943	AbS52943 Human tes
90	15.4	77.0	279	12	ADL86759	AdL86759 DNA up-re
91	15.4	77.0	279	12	ADL86760	AdL86760 DNA up-re
92	15.4	77.0	559	12	ACH91981	Ach91981 Human gen
93	15.4	77.0	769	6	ABK48683	Abk48683 Interleuk

c	94	15.4	77.0	1176	8	ABZ09924	Abz09924 Human 5'	167	15.2	76.0	747	12	ADG55209	Adg55209 Human Bcl1
c	95	15.4	77.0	1185	13	ADSI7323	Adsi7323 Rat liver	168	15.2	76.0	926	2	AAQ81698	Aaq81698 Human thy
c	96	15.4	77.0	1399	8	ABX05492	Abx05492 Human nov	169	15.2	76.0	926	2	AAQ40079	Aaq40079 Bcl1-XL ge
c	97	15.4	77.0	1623	2	AAx27946	Aax27946 Rat l(3)m	170	15.2	76.0	926	3	AAZ93614	Aaz93614 Bcl1-x gen
c	98	15.4	77.0	1636	5	AAQ02296	Aaq02296 Nicotiana	171	15.2	76.0	926	4	AAAS15189	Aas15189 Human bcl1
c	99	15.4	77.0	1777	8	ABX63743	Abx63743 Human cdn	172	15.2	76.0	926	4	AAQ50810	Aaq50810 Human bcl1
c	100	15.4	77.0	1840	10	ADBS59179	Adbs59179 Toxicity-r	173	15.2	76.0	926	6	ABK84766	Abk84766 Human cdn
c	101	15.4	77.0	1840	10	ADBS3879	Adbs3879 Primary r	174	15.2	76.0	926	6	ABT16641	Abt16641 Human bcl1
c	102	15.4	77.0	1924	12	ADQ84523	Adq84523 Human tum	175	15.2	76.0	926	10	ADDS6779	Add6779 Human bcl1
c	103	15.4	77.0	1926	4	AAK94134	Aak94134 Human ful	176	15.2	76.0	926	10	ADDS64187	Add64187 Human bcl1
c	104	15.4	77.0	1926	12	ADL30603	Adl30603 Full leng	177	15.2	76.0	926	11	ADI32104	Adi32104 Human cdn
c	105	15.4	77.0	2148	13	ADRO6522	Adro6522 Full leng	178	15.2	76.0	926	12	ADHS2630	Adhs2630 Human ant
c	106	15.4	77.0	2423	8	ABZ35902	Abz35902 Human sec	179	15.2	76.0	926	12	ADO19990	Ado19990 Human PRO
c	107	15.4	77.0	2521	5	AAAC67756	Aaac67756 DNA encod	180	15.2	76.0	926	12	ADP13351	Adp13351 Renal cel
c	108	15.4	77.0	2521	10	ADC32262	Adc32262 Human nov	181	15.2	76.0	1032	13	ADT46611	Adt46611 Bacterial
c	109	15.4	77.0	2522	10	ADB63450	Adb63450 Human cdn	c 182	15.2	76.0	1146	2	AAAT95382	Aat95382 DNA for h
c	110	15.4	77.0	2710	8	ABX34710	Abx34710 Human mdd	183	15.2	76.0	1236	5	AAQ02447	Aaq02447 Bcl1-XI-DT
c	111	15.4	77.0	2714	2	AAx27922	Aax27922 Mouse l(3	c 184	15.2	76.0	1302	2	AAAT95381	Aat95381 DNA for h
c	112	15.4	77.0	2918	5	AAAS83129	Aas83129 DNA encod	c 185	15.2	76.0	1302	2	AAV11651	Aav11651 Hepatitis
c	113	15.4	77.0	2922	2	AAx27923	Aax27923 Rat l(3)m	c 186	15.2	76.0	1360	12	ADO36027	Ado36027 Novel mou
c	114	15.4	77.0	3058	10	ADC30391	Adc30391 Human nov	187	15.2	76.0	1455	5	AAAS00250	Aas00250 LFn-Bcl-x
c	115	15.4	77.0	3058	13	ADRO7859	Adro7859 Full leng	188	15.2	76.0	1455	8	AAAL60717	Aal60717 Versinia
c	116	15.4	77.0	6127	6	ABSS5951	Abss5951 Human tes	189	15.2	76.0	1455	8	ACAS4358	Acas4358 Prokaryot
c	117	15.4	77.0	11259	4	ABLO2872	Ablo2872 Drosophill	190	15.2	76.0	1835	13	ADS60822	Ads60822 Bacterial
c	118	15.4	77.0	12789	6	AAAS16876	Aas16876 Human int	191	15.2	76.0	1897	3	AACT77290	Aac77290 Human ORF
c	119	15.4	77.0	31231	11	ACN44434	Acn44434 Human can	192	15.2	76.0	1944	13	ADA47980	Ada7980 Bacterial
c	120	15.4	77.0	32028	2	AAZ32028	Aaz32028 Human MET	c 193	15.2	76.0	2193	5	AAAH66319	Aah66319 C glutami
c	121	15.4	77.0	38186	2	AAZ32028	Aaz32028 Human MET	c 194	15.2	76.0	2312	6	AAAD33662	Aad33662 Human TRI
c	122	15.4	77.0	38186	5	AAQ90085	Aaq90085 AC004449	c 195	15.2	76.0	2316	4	AAAF71540	Aaf71540 Corynebac
c	123	15.4	77.0	43411	6	ABQ89169	Abq89169 Human ost	196	15.2	76.0	2502	8	ADA70916	Ada70916 Rice gene
c	124	15.4	77.0	59838	11	ACNA4982	Acna4982 Human gen	197	15.2	76.0	2575	12	ADO19866	Ado19866 Human PRO
c	125	15.4	77.0	96594	10	ADC85476	Adc85476 Human Mef	198	15.2	76.0	2575	13	ACN40740	Acn40740 Tumour-as
c	126	15.4	77.0	96595	9	ADA02996	Ada02996 Human Mef	199	15.2	76.0	2575	13	ADP54991	Adp54991 Human PRO
c	127	15.4	77.0	96595	10	ADB27234	Adb27234 Human Mef	200	15.2	76.0	2575	13	ADP24509	Adp24509 PRO polyP
c	128	15.4	77.0	96595	12	ADM74591	Adm74591 Human car	201	15.2	76.0	2598	12	ADQ97785	Adq97785 Human can
c	129	15.4	77.0	12767	13	ABDL32657	Abdl32657 Mouse can	202	15.2	76.0	2896	6	ABK89378	Abk89378 Human sec
c	130	15.4	77.0	182328	12	ADLO8128	Adlo8128 Human gen	203	15.2	76.0	3062	6	ABN99378	Abn99378 Human sec
c	131	15.4	77.0	233380	11	ACNA4282	Acna4282 Human gen	204	15.2	76.0	3110	5	AA572699	Aas72699 DNA encod
c	132	15.2	76.0	20	4	AAAC86401	Aac86401 Human bcl1	c 205	15.2	76.0	3591	4	ABL29414	AbL29414 Drosophil
c	133	15.2	76.0	20	4	AAAC86404	Aac86404 Human bcl1	c 206	15.2	76.0	4044	10	ADB69101	Adb69101 C. neofor
c	134	15.2	76.0	20	9	ADA24238	Ada24238 Human bcl1	207	15.2	76.0	4912	13	ADB85946	AdB85946 Human tum
c	135	15.2	76.0	209	2	AAH85853	Aah85853 Human sin	208	15.2	76.0	4926	13	ADR24490	Adr24490 Breast ca
c	136	15.2	76.0	209	2	AAH85852	Aah85852 Human sin	c 209	15.2	76.0	5511	8	ABT18892	Abt18892 Aspergill
c	137	15.2	76.0	237	12	ACH82413	Ach82413 Human gen	c 210	15.2	76.0	5574	8	ABT20712	Abt20712 Aspergill
c	138	15.2	76.0	337	10	ADK66037	Adk66037 Standardi	c 211	15.2	76.0	5713	8	ABT18298	Abt18298 Aspergill
c	139	15.2	76.0	338	3	AAK00549	Aak00549 Human sec	c 212	15.2	76.0	5713	8	ABT20114	Abt20114 Aspergill
c	140	15.2	76.0	340	2	AAAX40868	Aax40868 Human sec	213	15.2	76.0	5788	13	ADP22963	Adp22963 PRO polyP
c	141	15.2	76.0	357	9	ACH31711	Ach31711 Human bon	214	15.2	76.0	6104	3	AACT77046	Aac77046 Human ORF
c	142	15.2	76.0	492	9	ACH46093	Ach46093 Human inf	215	15.2	76.0	6177	10	ADF82008	Adf82008 Leukaemia
c	143	15.2	76.0	500	12	ACH68713	Ach68713 Human gen	c 216	15.2	76.0	6202	13	ADR65944	Adr65944 Human pro
c	144	15.2	76.0	505	6	ABN765010	Abn765010 Human ORP	217	15.2	76.0	6202	13	ADR66628	Adr66628 Human pro
c	145	15.2	76.0	557	4	AAI17049	Aai17049 Probe #69	218	15.2	76.0	7372	2	AAAX33182	Aax33182 Base sequ
c	146	15.2	76.0	557	4	ABA61283	Aba61283 Human foe	219	15.2	76.0	7666	13	ADR07802	Adr07802 Full leng
c	147	15.2	76.0	557	4	RAI41185	RAi41185 Probe #98	c 220	15.2	76.0	7713	8	ABT19518	Abt19518 Aspergill
c	148	15.2	76.0	557	4	ABA23108	Aba23108 Human bon	c 221	15.2	76.0	7713	8	ABT17704	Abt17704 Aspergill
c	149	15.2	76.0	557	4	AAK35472	Aak35472 Human bon	c 222	15.2	76.0	9327	8	ABT108958	Aat08958 Hepatitis
c	150	15.2	76.0	557	4	AAK09578	Aak09578 Human bra	c 223	15.2	76.0	9327	2	AAV66279	Aav66279 Recombina
c	151	15.2	76.0	557	4	ABSS35205	Abss35205 Human liv	c 224	15.2	76.0	9327	2	AAV56242	Aav56242 HGV sola
c	152	15.2	76.0	557	6	ABSO9820	Abso9820 Human gen	c 225	15.2	76.0	9327	2	AAAX16505	Aax16505 Polynucle
c	153	15.2	76.0	564	2	RAAT47667	Raat47667 PreproMF-	c 226	15.2	76.0	9327	2	AAAX02517	Aax02517 US5856134
c	154	15.2	76.0	599	6	ABK80930	Abk80930 Bacillus	c 227	15.2	76.0	9327	2	AAV82248	Aav82248 Hepatitis
c	155	15.2	76.0	636	4	AAH48169	Aah48169 Mutant bc	c 228	15.2	76.0	9391	2	AAAT15656	Aat15656 HGV-PNF 2
c	156	15.2	76.0	702	5	AAH43464	Aah43464 cDNA clon	c 229	15.2	76.0	9391	2	AAAT94168	Aat94168 Hepatitis
c	157	15.2	76.0	702	12	ADMA4594	Adma4594 Human apo	c 230	15.2	76.0	9392	2	AAAT08812	Aat08812 Hepatitis
c	158	15.2	76.0	702	13	ADSV74144	Adsv74144 Human Bcl1	c 231	15.2	76.0	9392	2	AAV66102	Aav66102 HGV-PNF21
c	159	15.2	76.0	735	2	AAAT08850	Aat08850 Hepatitis	c 232	15.2	76.0	9392	2	AAV656058	Aav656058 HGV sola
c	160	15.2	76.0	735	2	AAV66175	Aav66175 Consensus	c 233	15.2	76.0	9392	2	AAAX16351	Aax16351 Polynucle
c	161	15.2	76.0	735	2	AAV56138	Aav56138 HGV conse	c 234	15.2	76.0	9392	2	AAAX02334	Aax02334 US5856134
c	162	15.2	76.0	735	2	AAAX16389	Aax16389 Consensus	c 235	15.2	76.0	9392	2	AAV82093	Aav82093 Hepatitis
c	163	15.2	76.0	735	2	AAAX02413	Aax02413 US5856134	c 236	15.2	76.0	9395	2	AAAT76930	Aat76930 GR10 gen
c	164	15.2	76.0	735	2	AAV82131	Aav82131 Hepatitis	c 237	15.2	76.0	9395	5	AAAS15944	Aas15944 DNA encod
c	165	15.2	76.0	747	13	ADG65218	Adg65218 Human Bcl1	c 238	15.2	76.0	9395	13	ADC92820	Adc92820 Hepatitis
c	166	15.2	76.0	747	4	AAF30926	Aaf30926 Human Bcl1	c 239	15.2	76.0	9958	8	ACC46296	Acc46296 Human dit

240	15.2	76.0	36138	10	ADB74387	Adb74387 Mycobacte	C 313	14.8	74.0	991	3	AAH51424	Aah51424 Human UGT
241	15.2	76.0	44861	6	AAS20000	Aas20000 DNA encod	C 314	14.8	74.0	1083	9	AAH65200	Aah65200 C glutami
242	15.2	76.0	110000	2	AAZ01425_01	Continuation (2 of	C 315	14.8	74.0	1089	5	ADA02851	Ada02851 Mouse Cbx
243	15.2	76.0	110000	6	ABQ67196_0	ABQ67196 Listeria	C 316	14.8	74.0	1089	10	ADC85330	Adc85330 Mouse Cbx
244	15.2	76.0	110000	6	ABQ69245_25	Continuation (26 o	C 317	14.8	74.0	1089	10	ADC85330	Adc85330 Mouse Cbx
245	15.2	76.0	110000	13	ABQ32923_2	Continuation (3 of	C 318	14.8	74.0	1089	12	ADM74446	Adm74446 Murine ca
246	15.2	76.0	133833	11	ACN44956_2	Continuation (3 of	C 319	14.8	74.0	1092	11	ABD11566	Abd11566 Pseudomon
247	15.2	76.0	349980	5	AAH68528	Aah68528 Mouse gen	C 320	14.8	74.0	1134	11	ABD14157	Abd14157 Pseudomon
248	15.2	76.0	349980	6	ABQ81847	Aah68528 C glutami	C 321	14.8	74.0	1134	11	ABD14157	Abd14157 Pseudomon
249	15	75.0	19	10	ADP49386	Adf49386 Human BCL	C 322	14.8	74.0	1329	4	AAF67996	Aaf67996 Corynebact
250	15	75.0	19	10	ADP49800	Adf49800 Human BCL	C 323	14.8	74.0	1347	5	AAH68020	Aah68020 C glutami
251	15	75.0	60	6	ABN37341	Abn37341 Human spl	C 324	14.8	74.0	1404	8	ACA45511	Aca45511 Prokaryot
252	15	75.0	305	8	ABQ82914	Abq82914 Human lun	C 325	14.8	74.0	1407	2	AAH98049	Aah98049 Nucleotid
253	15	75.0	574	6	ABK34981	Abk34981 Human cdn	C 326	14.8	74.0	1410	4	AAH54353	Aah54353 Pseudomon
254	15	75.0	2357	4	AAK94271	Aak94271 Human ful	C 327	14.8	74.0	1410	8	ACA42733	Aca42733 Prokaryot
255	15	75.0	2357	12	ADL30867	Adl30867 Full leng	C 328	14.8	74.0	1413	9	ADA02850	Ada02850 Mouse Cbx
256	15	75.0	5279	6	ABS74269	Abs74269 Human cdn	C 329	14.8	74.0	1413	10	ADB72588	Adb72588 Mouse Cbx
257	15	75.0	5279	9	ACD25667	Acd25667 Human cdn	C 330	14.8	74.0	1413	10	ADC85329	Adc85329 Mouse Cbx
258	15	75.0	5303	12	ADQ18979	Adq18979 Human sof	C 331	14.8	74.0	1413	10	ADM74445	Adm74445 Murine ca
259	15	75.0	5463	6	ABS74267	Abs74267 Human cdn	C 332	14.8	74.0	1413	12	ADM74445	Adm74445 Murine ca
260	15	75.0	5463	9	ACD25665	Acd25665 Human cdn	C 333	14.8	74.0	1465	4	AAI64629	Aai64629 Mouse MIT
261	15	75.0	5482	3	AAA09255	Aaa09255 Human alp	C 334	14.8	74.0	1498	11	ADL65516	Adl65516 C. glutam
262	15	75.0	5482	4	AAS01413	Aas01413 Human sec	C 335	14.8	74.0	1500	11	ABD17747	Abd17747 Pseudomon
263	15	75.0	5482	5	AAF57550	Aaf57550 Human cal	C 336	14.8	74.0	1506	8	ABZ25581	Abz25581 Human tra
264	15	75.0	5482	6	ABS74268	Abs74268 Human cdn	C 337	14.8	74.0	1563	12	ADO29802	Ado29802 Human GPC
265	15	75.0	5482	9	ACD25666	Acd25666 Human cdn	C 338	14.8	74.0	1572	4	AAI64630	Aai64630 Mouse MIT
266	15	75.0	5583	12	ADQ23337	Adq23337 Human sof	C 339	14.8	74.0	1678	10	ADP57270	Adp57270 Human gen
267	15	75.0	5730	13	ABD32813	Abd32813 Human can	C 340	14.8	74.0	1678	10	ADP57266	Adp57266 Human gen
268	15	75.0	5730	13	ABD32812	Abd32812 Human can	C 341	14.8	74.0	1738	2	AAQ63181	Aaq63181 Alpha 1b
269	15	75.0	30752	11	ACN44344	Acn44344 Mouse gen	C 342	14.8	74.0	1738	2	AAQ62817	Aaq62817 Genomic s
270	15	75.0	140152	12	ADP03002	Adp03002 Human hou	C 343	14.8	74.0	1738	2	AAAF2406	Aaf2406 Human alp
271	15	75.0	140152	13	ADS88500	Ads88500 Human hou	C 344	14.8	74.0	1738	2	AAAT03128	Aat03128 Alpha-1B
272	15	75.0	161051	13	ABD32811	Abd32811 Human can	C 345	14.8	74.0	1738	10	ACA56804	Aca56804 Human sig
273	15	75.0	166181	12	ADQ18633	Adq18633 Human sof	C 346	14.8	74.0	1738	12	ADL56600	Adl56600 Human pol
274	15	75.0	166181	12	ADQ18633	Adq18633 Human sof	C 347	14.8	74.0	1786	10	ABZ42621	Abz42621 Human alp
275	14.8	74.0	29	11	ADM33364	Adm33364 Immunoglo	C 348	14.8	74.0	1803	5	AAAD18907	Aad18907 Human dia
276	14.8	74.0	29	11	ADM33363	Adm33363 Immunoglo	C 349	14.8	74.0	1803	5	AAH78387	Aah78387 DNA encod
277	14.8	74.0	29	11	ADM33841	Adm33841 Human IGG	C 350	14.8	74.0	1859	2	AAZ42244	Aaz42244 Human nor
278	14.8	74.0	29	11	ADM33840	Adm33840 Human IGG	C 351	14.8	74.0	1886	10	ADA53915	Ada53915 Human cod
279	14.8	74.0	29	13	ADR48971	Adr48971 Human IGG	C 352	14.8	74.0	1889	11	ADM02361	Adm02361 Human cdn
280	14.8	74.0	29	13	ADR48972	Adr48972 Human IGG	C 353	14.8	74.0	2067	4	AAI64628	Aai64628 Mouse MIT
281	14.8	74.0	271	10	AAAD61365	AAAD61365 BS136 spe	C 354	14.8	74.0	2104	10	ADB58064	Adb58064 Toxicity-
282	14.8	74.0	317	10	ACD94733	Acn44344 Mouse gen	C 355	14.8	74.0	2104	10	ADB52541	Adb52541 Primarity
283	14.8	74.0	325	10	ACD92995	Acn44344 Mouse gen	C 356	14.8	74.0	2104	10	ABT41809	Abt41809 Toxicity
284	14.8	74.0	325	10	ACD93074	Acn44344 Mouse gen	C 357	14.8	74.0	2104	12	ADP72572	Adp72572 Renal tox
285	14.8	74.0	350	10	ACD93076	Acn44344 Mouse gen	C 358	14.8	74.0	2125	4	AAI64631	Aai64631 Mouse MIT
286	14.8	74.0	354	6	ABN16011	Abn16011 Human ORF	C 359	14.8	74.0	2151	12	ADP19845	Adp19845 Rat Oatpl
287	14.8	74.0	359	8	ABX54712	Abx54712 Bovine ES	C 360	14.8	74.0	2196	4	AAI64627	Aai64627 Mouse MIT
288	14.8	74.0	429	9	ACH26780	Ach26780 Human adu	C 361	14.8	74.0	2244	8	ABX10236	Abx10236 Human cdn
289	14.8	74.0	447	11	ABD17534	Abd17534 Pseudomon	C 362	14.8	74.0	2244	5	ADG39795	Adg39795 Human cdn
290	14.8	74.0	474	12	ACH89272	Ach89272 Human gen	C 363	14.8	74.0	2247	5	AAH82595	Aah82595 DNA encod
291	14.8	74.0	491	9	ACH22604	Ach22604 Human adu	C 364	14.8	74.0	2258	10	ADB62055	Adb62055 Human cdn
292	14.8	74.0	497	4	AAAF72120	Aaf72120 Corynebact	C 365	14.8	74.0	2370	4	AAH180671	Aah180671 Human pol
293	14.8	74.0	501	2	AAQ97709	Aaq97709 Branched-	C 366	14.8	74.0	2405	4	AAH17812	Aah17812 Human cdn
294	14.8	74.0	558	11	ABD13850	Abd13850 Pseudomon	C 367	14.8	74.0	2405	13	ACN37731	Acn37731 Tumour-sa
295	14.8	74.0	570	12	ADN98705	Adn98705 Pseudomon	C 368	14.8	74.0	2434	4	AAK94695	Aak94695 Human ful
296	14.8	74.0	570	12	ADO00274	Ado00274 Novel hum	C 369	14.8	74.0	2434	12	ADL31683	Adl31683 Full leng
297	14.8	74.0	589	12	ACH75537	Ach75537 Human gen	C 370	14.8	74.0	2469	12	ADO64622	Ado64622 Novel hum
298	14.8	74.0	601	4	AAK68753	Aak68753 Human imm	C 371	14.8	74.0	2485	12	ADO35406	Ado35406 Novel mou
299	14.8	74.0	650	10	AD34132	Ad34132 Mouse mit	C 372	14.8	74.0	2537	13	ABD33166	Abd33166 Murine ca
300	14.8	74.0	652	12	ADQ21080	Adq21080 Human sof	C 373	14.8	74.0	2579	4	ABL26294	AbL26294 Drosophil
301	14.8	74.0	661	11	ACN45189	Acn45189 Mouse mRN	C 374	14.8	74.0	2771	4	ABL14381	AbL14381 Drosophil
302	14.8	74.0	754	8	ABZ51865	Abz51865 Aspergill	C 375	14.8	74.0	2884	13	ACN42618	Acn42618 Human dta
303	14.8	74.0	755	3	AAH51423	Aah51423 Human UGT	C 376	14.8	74.0	3017	10	AAAD61370	AAAD61370 BS136 spe
304	14.8	74.0	763	10	ABX94906	Abx94906 P. aureogi	C 377	14.8	74.0	3078	4	ABL08368	AbL08368 Drosophil
305	14.8	74.0	765	9	ABT43730	Abt43730 Molecule	C 378	14.8	74.0	3102	8	ABZ24009	Abz24009 Mouse adi
306	14.8	74.0	792	13	ADRS1432	Adrs1432 Anti-biof	C 379	14.8	74.0	3102	8	ABZ24027	Abz24027 Mouse adi
307	14.8	74.0	798	2	AAH98050	Aah98050 Nucleotid	C 380	14.8	74.0	3102	3	AAAF18096	Aaf18096 Nuc cand
308	14.8	74.0	813	4	AAK56761	Aak56761 Human imm	C 381	14.8	74.0	3141	2	AAH98041	Aah98041 Nucleotid
309	14.8	74.0	835	10	AD34582	Ad34582 Mouse mit	C 382	14.8	74.0	3150	11	ABD11300	Abd11300 Pseudomon
310	14.8	74.0	918	12	ADQ60122	Adq60122 Murine-de	C 383	14.8	74.0	3283	2	AAZ33572	Aaz33572 Human bre
311	14.8	74.0	961	4	ABL12493	AbL12493 Drosophil	C 384	14.8	74.0	3405	3	AAF21754	Aaf21754 Human bre
312	14.8	74.0	990	12	ADQ60124	Adq60124 His tag-T	C 385	14.8	74.0	3506	10	AAAD61371	AAAD61371 BS136 spe

386	14.8	74.0	3889	6	ABS70382	AbS70382 Human bon	c 459	14.8	74.0	164702	8	ADB20845	Adb20845 MRP1 base
387	14.8	74.0	4005	4	AAC85088	Aac85088 Atheroesc	c 460	14.8	74.0	164702	10	ADB87934	Adb87934 Human UGT
388	14.8	74.0	4005	11	ADM29576	Adm29576 Human ath	c 461	14.8	74.0	164702	10	ADB96917	Adb96917 Human MDR
389	14.8	74.0	4120	4	AAI60250	Aai60250 Human pol	c 462	14.8	74.0	164702	10	ADB92108	Adb92108 Human MDR
390	14.8	74.0	4140	4	ABL04087	AbL04087 Drosophil	c 463	14.8	74.0	204621	11	ACN44486	Acn44486 Human gen
c 391	14.8	74.0	4193	5	AAS85066	Aas85066 DNA encod	c 464	14.8	74.0	254087	11	ACN43996	Acn43996 Mouse gen
c 392	14.8	74.0	4493	12	ADQ63030	Adq63030 Novel hum	c 465	14.8	74.0	304905	11	ADP75180	Adp75180 Human End
c 393	14.8	74.0	4845	4	ABL20700	AbL20700 Drosophil	c 466	14.8	74.0	349980	5	AAH68533	Aah68533 C glutami
394	14.8	74.0	5338	4	ABL14380	AbL14380 Drosophil	c 467	14.8	74.0	349980	5	AAH64966	Aah64966 C glutami
395	14.8	74.0	6108	6	AAI39666	Aai39666 Human sec	c 468	14.8	74.0	349980	5	ACD65499	AcD65499 HCV minus
396	14.8	74.0	6309	12	ADN05387	Adn05387 Antipsoi	c 469	14.8	74.0	349980	5	ACD57170	AcD57170 HCV DNazy
397	14.8	74.0	6356	12	ADQ24996	Adq24996 Human sof	c 470	14.8	74.0	349980	5	ADH187105	Adh187105 HCV DNazy
398	14.8	74.0	6600	12	ADH71899	Adh71899 Human sof	c 471	14.8	74.0	349980	5	ADI82958	Adi82958 HCV DNazy
399	14.8	74.0	6718	2	AAX58619	Aax58619 Human act	c 472	14.8	74.0	349980	5	AAH63817	Aah63817 Primer us
400	14.8	74.0	6719	10	ADH29072	Adh29072 Human chr	c 473	14.8	74.0	349980	5	AAH39716	Aah39716 Human SNP
401	14.8	74.0	6719	12	ADF72343	Adf72343 Human sup	c 474	14.8	74.0	349980	5	ADH19076	Adh19076 Caffeine
c 402	14.8	74.0	6943	4	AAS42087	Aas42087 Genomic s	c 475	14.8	74.0	349980	5	ABS72179	AbS72179 Human gen
403	14.8	74.0	7025	11	ACN44487	Acn44487 Human mRN	c 476	14.8	74.0	349980	5	AAH20184	Aah20184 Human sec
c 404	14.8	74.0	7119	10	ADG42152	Adg42152 Human bra	c 477	14.8	74.0	349980	5	ADP57917	Adp57917 Maize car
c 405	14.8	74.0	7586	2	AAX58621	Aax58621 Human act	c 478	14.8	74.0	349980	5	AAH61358	Aah61358 BS136 spe
406	14.8	74.0	8041	12	ADQ25072	Adq25072 Human sof	c 479	14.8	74.0	349980	5	ABN17867	Abn17867 Human ORF
407	14.8	74.0	8249	6	AAS94883	Aas94883 Human DNA	c 480	14.8	74.0	349980	5	AAH98149	Aah98149 Nucleotid
408	14.8	74.0	8297	13	ACN39031	Acn39031 Tumour-as	c 481	14.8	74.0	349980	5	ABQ67402	Abq67402 Listeria
c 409	14.8	74.0	8382	4	ABL04086	AbL04086 Drosophil	c 482	14.8	74.0	349980	5	ADE59448	Ade59448 Rat gene
410	14.8	74.0	8748	4	ABL12492	AbL12492 Drosophil	c 483	14.8	74.0	349980	5	ADD5645	Add5645 Rat gene
411	14.8	74.0	8752	12	ADM32771	Adm32771 Nucleotid	c 484	14.8	74.0	349980	5	AAH10407	Aah10407 Human bre
c 412	14.8	74.0	12535	4	ABL20360	AbL20360 Drosophil	c 485	14.8	74.0	349980	5	ABV15361	Abv15361 Human pro
413	14.8	74.0	12989	4	ABK42602	Abk42602 Genomic s	c 486	14.8	74.0	349980	5	AAH88734	Aah88734 Human dig
414	14.8	74.0	12989	9	ADB60758	Adb60758 Connectiv	c 487	14.8	74.0	349980	5	AAH31768	Aah31768 Human liv
c 415	14.8	74.0	14040	4	AAH07517	Aah07517 Human rep	c 488	14.8	74.0	349980	5	ABN90123	Abn90123 Human liv
c 416	14.8	74.0	14040	4	AAH02790	Aah02790 Human rep	c 489	14.8	74.0	349980	5	ADJ14890	Adj14890 Human liv
c 417	14.8	74.0	14040	4	ABA08209	AbA08209 Human ova	c 490	14.8	74.0	349980	5	AAQ35079	Aaq35079 HCV envel
418	14.8	74.0	19929	4	AAH07279	Aah07279 Human rep	c 491	14.8	74.0	349980	5	AAH85782	Aah85782 Human pol
419	14.8	74.0	19929	4	ABL98825	AbL98825 Human tes	c 492	14.8	74.0	349980	5	ADP34516	Adp34516 Mouse mit
420	14.8	74.0	20907	4	AAH07278	Aah07278 Human rep	c 493	14.8	74.0	349980	5	AAH48102	Aah48102 Zea mays
c 421	14.8	74.0	20907	4	ABL98824	AbL98824 Human tes	c 494	14.8	74.0	349980	5	ACH46154	Ach46154 Human pro
c 422	14.8	74.0	22478	9	ADA02849	Ada02849 Mouse Cbx	c 495	14.8	74.0	349980	5	ACH46473	Ach46473 Human inf
c 423	14.8	74.0	22478	10	ADB72587	Adb72587 Mouse Cbx	c 496	14.8	74.0	349980	5	ABV23780	Abv23780 Human pro
c 424	14.8	74.0	22478	10	ADC85328	Adc85328 Human Fgf	c 497	14.8	74.0	349980	5	ABV23961	Abv23961 Human pro
c 425	14.8	74.0	22478	12	ADM74444	Adm74444 Murine ca	c 498	14.8	74.0	349980	5	ABV29655	Abv29655 Human pro
426	14.8	74.0	23328	9	ADA02918	Ada02918 Human FUS	c 499	14.8	74.0	349980	5	ABV29846	Abv29846 Human pro
427	14.8	74.0	23328	10	ADB72656	Adb72656 Human FUS	c 500	14.8	74.0	349980	5	AAH19988	Aah19988 Human bre
428	14.8	74.0	23328	10	ADC85398	Adc85398 Human Fus	c 501	14.8	74.0	349980	5	AAH98150	Aah98150 Nucleotid
429	14.8	74.0	23328	12	ADM74513	Adm74513 Human car	c 502	14.8	74.0	349980	5	ACH78637	Ach78637 Human gen
c 430	14.8	74.0	23367	12	ADQ97939	Adq97939 Mouse can	c 503	14.8	74.0	349980	5	AAH87912	Aah87912 Mouse B5T
c 431	14.8	74.0	27589	9	ADA02924	Ada02924 Human RAS	c 504	14.8	74.0	349980	5	ABQ67580	Abq67580 Listeria
432	14.8	74.0	27589	10	ADB72662	Adb72662 Human RAS	c 505	14.8	74.0	349980	5	ABV57573	Abv57573 Human pro
433	14.8	74.0	27589	10	ADC85404	Adc85404 Human Ras	c 506	14.8	74.0	349980	5	ABV57573	Abv57573 Murine ge
434	14.8	74.0	27589	12	ADM74519	Adm74519 Human car	c 507	14.8	74.0	349980	5	ABN60829	Abn60829 Human can
c 435	14.8	74.0	32050	11	ACN444376	Acn444376 Mouse gen	c 508	14.8	74.0	349980	5	ADQ55346	Adq55346 Novel can
c 436	14.8	74.0	34261	13	ABD33518	Abd33518 Murine ca	c 509	14.8	74.0	349980	5	ABV50807	Abv50807 Human pro
437	14.8	74.0	34683	13	ABD33165	Abd33165 Murine ca	c 510	14.8	74.0	349980	5	ABL67456	AbL67456 Thyroid c
c 438	14.8	74.0	42235	2	AAX98035	Aax98035 Nucleotid	c 511	14.8	74.0	349980	5	ABL67043	AbL67043 Thyroid c
c 439	14.8	74.0	42519	4	AAK81318	Aak81318 Human imm	c 512	14.8	74.0	349980	5	ABN94667	Abn94667 Gene #116
440	14.8	74.0	49744	6	ABK12807	Abk12807 Human tum	c 513	14.8	74.0	349980	5	ADQ78597	Adq78597 Novel can
441	14.8	74.0	57130	8	ABQ77243	Abq77243 Human MAR	c 514	14.8	74.0	349980	5	ABL96321	AbL96321 Nucleotid
442	14.8	74.0	67384	11	ACN44756	Acn44756 Mouse gen	c 515	14.8	74.0	349980	5	ADK69799	Adk69799 Hepatitis
443	14.8	74.0	68495	11	ACN443553	Acn443553 Human can	c 516	14.8	74.0	349980	5	AAQ35077	Aaq35077 HCV envel
c 444	14.8	74.0	77941	11	ACN44320	Acn44320 Mouse gen	c 517	14.8	74.0	349980	5	AAQ35078	Aaq35078 HCV envel
445	14.8	74.0	79640	13	ABD33007	Abd33007 Mouse can	c 518	14.8	74.0	349980	5	ABV44974	Abv44974 Human pro
446	14.8	74.0	87749	11	ACN45026	Acn45026 Human gen	c 519	14.8	74.0	349980	5	ABV35911	Abv35911 Human pro
c 447	14.8	74.0	96499	11	ACN45188	Acn45188 Mouse gen	c 520	14.8	74.0	349980	5	ABV45211	Abv45211 Human pro
c 448	14.8	74.0	108916	13	ABD32804_5	Abd32804_5 of	c 521	14.8	74.0	349980	5	ACH79252	Ach79252 Human gen
c 449	14.8	74.0	110000	12	ADN46845_08	Adn46845_08 of	c 522	14.8	74.0	349980	5	AAH21784	Aah21784 Synthesis
c 450	14.8	74.0	110000	12	ADN47591_12	Adn47591_12 of	c 523	14.8	74.0	349980	5	AAH21784	Aah21784 Synthesis
c 451	14.8	74.0	110000	12	ADN46123_08	Adn46123_08 of	c 524	14.8	74.0	349980	5	AAH21784	Aah21784 Synthesis
452	14.8	74.0	110000	12	ADN47209_12	Adn47209_12 of	c 525	14.8	74.0	349980	5	AAH21784	Aah21784 Synthesis
c 453	14.8	74.0	110000	12	ADN46464_08	Adn46464_08 of	c 526	14.8	74.0	349980	5	AAH21784	Aah21784 Synthesis
454	14.8	74.0	110000	12	ADN47960_12	Adn47960_12 of	c 527	14.8	74.0	349980	5	AAH21784	Aah21784 Synthesis
c 455	14.8	74.0	110000	13	ABD32804_4	Abd32804_4 of	c 528	14.8	74.0	349980	5	AAH21784	Aah21784 Synthesis
456	14.8	74.0	111084	12	ADQ18808	Adq18808 Human sof	c 529	14.8	74.0	349980	5	AAH21784	Aah21784 Synthesis
c 457	14.8	74.0	112460	6	ABK83567	Abk83567 Human cdn	c 530	14.8	74.0	349980	5	AAH21784	Aah21784 Synthesis
c 458	14.8	74.0	164702	8	ACF62730	AcF62730 Cancer ba	c 531	14.8	74.0	349980	5	AAH21784	Aah21784 Synthesis

532	14.4	72.0	607	4	AAK14587	Aak14587 Human bra	605	14.4	72.0	1617	12	ADQ97661	Adq97661 Mouse can
533	14.4	72.0	607	4	ABS39903	Abs39903 Human liv	606	14.4	72.0	1697	4	AAC83979	Aac83979 Murine or
534	14.4	72.0	607	5	AAI06810	Aai06810 Probe #68	C 607	14.4	72.0	1790	5	AAS68959	Aas68959 DNA encod
535	14.4	72.0	607	6	ABS14350	Abs14350 Human gen	C 608	14.4	72.0	1791	2	AAK98146	Aak98146 Nucleotid
536	14.4	72.0	622	3	AAF12782	Aaf12782 Aspergill	C 609	14.4	72.0	1791	11	ABD06295	Abd06295 Pseudomon
537	14.4	72.0	623	3	AAF08941	Aaf08941 Fusarium	C 610	14.4	72.0	1801	4	ABA82022	Aba82022 Wound hea
538	14.4	72.0	629	8	ABZ51524	Abz51524 Aspergill	C 611	14.4	72.0	1829	4	AAK94866	Aak94866 Human ful
539	14.4	72.0	632	5	ABV05941	Abv05941 Human pro	C 612	14.4	72.0	1829	12	ADL32015	Adl32015 Full leng
540	14.4	72.0	634	5	AAS80637	Aas80637 DNA encod	C 613	14.4	72.0	1897	5	AAK87907	Aak87907 Rat Bst o
541	14.4	72.0	669	10	ADG25169	Adg25169 HCV plas	C 614	14.4	72.0	1911	5	ADL63060	Adl63060 Human ova
542	14.4	72.0	674	4	AAK53005	Aak53005 Human pol	C 615	14.4	72.0	1932	12	ADQ96385	Adq96385 T cell ac
543	14.4	72.0	693	4	AAK52021	Aak52021 Human pol	C 616	14.4	72.0	1932	12	ADQ96387	Adq96387 T cell ac
544	14.4	72.0	716	5	ABV15110	Abv15110 Human pro	C 617	14.4	72.0	1961	11	ADM03562	Adm03562 Human cdn
545	14.4	72.0	718	6	ABQ51059	Abq51059 CEGP1 pro	C 618	14.4	72.0	1979	4	AAI13910	Aai13910 Probe #38
546	14.4	72.0	727	6	ABK34370	Abk34370 Human cdn	C 619	14.4	72.0	1979	4	ABA55622	Aba55622 Human foe
547	14.4	72.0	746	8	ABZ76720	Abz76720 5' flanki	C 620	14.4	72.0	1979	4	AAI135277	Aai135277 Probe #39
548	14.4	72.0	829	4	AAK93801	Aak93801 Human cdn	C 621	14.4	72.0	1979	4	ABA45144	Aba45144 Human bra
549	14.4	72.0	829	4	AAK92352	Aak92352 Human cdn	C 622	14.4	72.0	1979	4	ABA25318	Aba25318 Probe #37
550	14.4	72.0	829	12	ADL28779	Adl28779 5' end of	C 623	14.4	72.0	1979	4	AAK29317	Aak29317 Human bon
551	14.4	72.0	829	12	ADL30228	Adl30228 3' end of	C 624	14.4	72.0	1979	4	AAK03850	Aak03850 Human bra
552	14.4	72.0	831	8	ACA42533	Aca42533 Prokaryot	C 625	14.4	72.0	1979	4	ABS28937	Abs28937 Human liv
553	14.4	72.0	845	11	ACN80605	Acn80605 Breast ca	C 626	14.4	72.0	1979	5	AAI03779	Aai03779 Probe #37
554	14.4	72.0	852	9	ADB83227	Adb83227 Human cdn	C 627	14.4	72.0	1979	6	ABS03875	Abs03875 Human gen
555	14.4	72.0	917	13	ADQ86739	Adq86739 Human tum	C 628	14.4	72.0	1992	2	AAO10895	Aao10895 Encodes X
556	14.4	72.0	917	13	ADQ84357	Adq84357 Human tum	C 629	14.4	72.0	2071	10	ADF90779	Adf90779 Human hep
557	14.4	72.0	917	13	ADQ85641	Adq85641 Human tum	C 630	14.4	72.0	2114	11	ADM01582	Adm01582 Human cdn
558	14.4	72.0	940	10	ADC86560	Adc86560 Human GPC	C 631	14.4	72.0	2128	2	AAK22400	Aak22400 Human liv
559	14.4	72.0	960	4	ABK50949	Abk50949 DNA encod	C 632	14.4	72.0	2135	3	AAK65395	Aak65395 Human car
560	14.4	72.0	974	4	ABK50970	Abk50970 DNA encod	C 633	14.4	72.0	2157	9	AAK62509	Aak62509 Human tra
561	14.4	72.0	981	6	AAK42576	Aak42576 Partial s	C 634	14.4	72.0	2158	10	ADF90866	Adf90866 Human hep
562	14.4	72.0	989	4	AAK08456	Aak08456 Human sec	C 635	14.4	72.0	2370	4	AAI80671	Aai80671 Human pol
563	14.4	72.0	996	2	AAK98147	Aak98147 Nucleotid	C 636	14.4	72.0	2373	4	ABL23063	AbL23063 Drosophill
564	14.4	72.0	998	4	AAI11882	Aai11882 Probe #18	C 637	14.4	72.0	2409	10	ABE15660	Abe15660 Human str
565	14.4	72.0	998	4	ABA35583	Aba35583 Human foe	C 638	14.4	72.0	2537	5	AAK90073	Aak90073 DNA encod
566	14.4	72.0	998	4	AAI33209	Aai33209 Probe #18	C 639	14.4	72.0	2565	3	AAK26415	Aak26415 cDNA enco
567	14.4	72.0	998	4	AAH99212	Aah99212 Human pro	C 640	14.4	72.0	2573	12	ADQ64905	Adq64905 Novel hum
568	14.4	72.0	998	4	ABA33164	Aba33164 Human bre	C 641	14.4	72.0	2577	6	AAK45289	Aak45289 Human KCN
569	14.4	72.0	998	4	ABA23338	Aba23338 Probe #18	C 642	14.4	72.0	2605	12	ADH22610	Adh22610 cDNA enco
570	14.4	72.0	998	4	AAK27308	Aak27308 Human bon	C 643	14.4	72.0	2861	5	AAH21506	Aah21506 Human ret
571	14.4	72.0	998	4	AAK01849	Aak01849 Human bra	C 644	14.4	72.0	3017	10	AAK61370	Aak61370 BS136 spe
572	14.4	72.0	998	4	ABS26882	Abs26882 Human liv	C 645	14.4	72.0	3061	10	ADB58678	Adb58678 Toxicity-
573	14.4	72.0	998	5	AAI01820	Aai01820 Probe #18	C 646	14.4	72.0	3061	10	ABE53365	Abe53365 Primary f
574	14.4	72.0	998	6	ABS01828	Abs01828 Human gen	C 647	14.4	72.0	3072	12	ADH22608	Adh22608 cDNA enco
575	14.4	72.0	998	10	ADF59853	Adf59853 Human con	C 648	14.4	72.0	3179	13	ADR06816	Adr06816 Full leng
576	14.4	72.0	1021	6	AAK41732	Aak41732 Human con	C 649	14.4	72.0	3283	2	AAK23572	Aak23572 Human bre
577	14.4	72.0	1106	5	AAK93245	Aak93245 DNA encod	C 650	14.4	72.0	3382	5	ABA20999	Aba20999 Human ner
578	14.4	72.0	1155	11	ABD16726	Abd16726 Pseudomon	C 651	14.4	72.0	3383	5	ABA20998	Aba20998 Human ner
579	14.4	72.0	1228	9	AAK57527	Aak57527 Human enz	C 652	14.4	72.0	3383	5	ABA20998	Aba20998 Human ner
580	14.4	72.0	1238	8	AAK51550	Aak51550 Human BCA	C 653	14.4	72.0	3506	10	AAK61371	Aak61371 BS136 spe
581	14.4	72.0	1251	5	AAH64941	Aah64941 Human sec	C 654	14.4	72.0	3607	13	ACN42696	Acn42696 Human dia
582	14.4	72.0	1258	4	AAH99842	Aah99842 Human pro	C 655	14.4	72.0	3654	12	ADQ64392	Adq64392 Novel hum
583	14.4	72.0	1264	2	AAV08832	Aav08832 Gene No.	C 656	14.4	72.0	3697	4	AAH98403	Aah98403 Human EST
584	14.4	72.0	1298	12	ADQ80750	Adq80750 Porcine e	C 657	14.4	72.0	3756	13	ADS16306	Ads16306 Human vol
585	14.4	72.0	1319	8	AAK51545	Aak51545 Human BCA	C 658	14.4	72.0	3777	8	ABZ24713	Abz24713 Human pot
586	14.4	72.0	1340	4	AAI23127	Aai23127 Probe #13	C 659	14.4	72.0	3889	6	ABS70382	Abs70382 Human bon
587	14.4	72.0	1340	4	ABA68220	Aba68220 Human foe	C 660	14.4	72.0	4005	4	AAC85088	Aac85088 Atheroscl
588	14.4	72.0	1340	4	AAI48435	Aai48435 Probe #17	C 661	14.4	72.0	4005	11	ADM29576	Adm29576 Human ach
589	14.4	72.0	1340	4	ABA50280	Aba50280 Human bre	C 662	14.4	72.0	4327	6	ABQ70944	Abq70944 Liesteria
590	14.4	72.0	1340	4	ABA35230	Aba35230 Probe #13	C 663	14.4	72.0	5442	4	ABL23062	AbL23062 Drosophill
591	14.4	72.0	1340	4	AAK42336	Aak42336 Human bon	C 664	14.4	72.0	5776	4	AAK74386	Aak74386 Human imm
592	14.4	72.0	1340	4	AAK16601	Aak16601 Human bra	C 665	14.4	72.0	5796	5	AAK30041	Aak30041 Human imm
593	14.4	72.0	1340	4	ABA31965	Aba31965 Human liv	C 666	14.4	72.0	5796	10	ADB33378	Adb33378 Human nov
594	14.4	72.0	1340	5	AAI08782	Aai08782 Probe #87	C 667	14.4	72.0	5945	12	ABD16307	Abd16307 Human nuc
595	14.4	72.0	1340	6	ABS16411	Abs16411 Human gen	C 668	14.4	72.0	5914	4	AAK86108	Aak86108 Human imm
596	14.4	72.0	1374	5	AAH67569	Aah67569 C glutami	C 669	14.4	72.0	5914	5	AAK30039	Aak30039 Human lun
597	14.4	72.0	1385	2	AAV80630	Aav80630 Kidney in	C 670	14.4	72.0	5914	10	ADB33376	Adb33376 Human nov
598	14.4	72.0	1407	2	AAK22401	Aak22401 Human liv	C 671	14.4	72.0	5919	12	ADO30968	Ado30968 Human Pol
599	14.4	72.0	1470	5	AAK65206	Aak65206 DNA* encod	C 672	14.4	72.0	6108	6	AAK139666	Aak139666 Human sec
600	14.4	72.0	1501	13	ADT66622	Adt66622 Rat splic	C 673	14.4	72.0	6239	4	AAK76233	Aak76233 Human imm
601	14.4	72.0	1539	13	ACN37738	Acn37738 Tumour-as	C 674	14.4	72.0	6266	6	ABA97392	Aba97392 Human p53
602	14.4	72.0	1549	4	AAH17040	Aah17040 Human cdn	C 675	14.4	72.0	6266	13	ACN39802	Acn39802 Tumour-as
603	14.4	72.0	1556	4	AAK72101	Aak72101 Corynebac	C 676	14.4	72.0	6309	12	ADN05387	Adn05387 Anti-psori
604	14.4	72.0	1612	12	ADJ39588	Adj39588 Plant cdn	C 677	14.4	72.0	6356	12	ADQ24996	Adq24996 Human sof

678 14.4 72.0 6558 10 ADE62223 Ade62223 Human gen
c 679 14.4 72.0 6600 12 ADH71899 Adh71899 Human gen
680 14.4 72.0 6789 10 ADD47934 Add47934 Human gen
c 681 14.4 72.0 7222 8 ABT42544 Abt42544 Human nuc
c 682 14.4 72.0 7592 13 ACN37313 Acn37313 Tumour-as
c 683 14.4 72.0 7647 2 AAV15519 Aavi15519 Hamster o
c 684 14.4 72.0 8277 4 ABL18402 Abl18402 Drosophill
c 685 14.4 72.0 8382 4 AAK70731 Aak70731 Human imm
c 686 14.4 72.0 10347 4 AAK74385 Aak74385 Human imm
c 687 14.4 72.0 10394 9 AAL61117 Aal61117 Human tum
c 688 14.4 72.0 10394 12 ADM98082 Adm98082 Human tum
c 689 14.4 72.0 10437 4 AAS41709 Aas41709 Genomic s
c 690 14.4 72.0 12525 6 AAD33319 Aad33319 Rat C3b/c
c 691 14.4 72.0 12620 5 ABA16691 Aba16691 Human ner
c 692 14.4 72.0 16326 4 AAK69677 Aak69677 Human imm
c 693 14.4 72.0 18022 12 ADQ03148 Adq03148 Fusion tr
c 694 14.4 72.0 19174 4 AAK81253 Aak81253 Human imm
c 695 14.4 72.0 20633 13 ABD33620 Abd33620 Human can
c 696 14.4 72.0 26372 4 AAK77103 Aak77103 Human imm
c 697 14.4 72.0 28918 4 ABL14456 Abl14456 Drosophill
c 698 14.4 72.0 31203 4 AAK81254 Aak81254 Human imm
c 699 14.4 72.0 32985 9 ADA02759 Ada02759 Mouse Run
c 700 14.4 72.0 32985 10 ADB72497 Adb72497 Mouse Run
c 701 14.4 72.0 34668 10 ACC00044 Acc00044 Nucleotid
c 702 14.4 72.0 37265 11 ACN43880 Acn43880 Mouse gen
c 703 14.4 72.0 40050 9 ADA02585 Ada02585 Mouse Ics
c 704 14.4 72.0 40050 10 ADB72323 Adb72323 Mouse Ics
c 705 14.4 72.0 40050 10 ADE95833 Ade95833 Mouse ics
c 706 14.4 72.0 40352 2 AAV02032 Aav02032 MAGE-B cl
c 707 14.4 72.0 40558 12 ADJ47542 Adj47542 Human H19
c 708 14.4 72.0 42379 12 ADQ97660 Adq97660 Mouse can
c 709 14.4 72.0 42979 4 ABL20870 Abl20870 Drosophill
c 710 14.4 72.0 49272 2 AAV35000 Aav35000 Mycobacte
c 711 14.4 72.0 51323 13 ABD32784 Abd32784 Mouse can
c 712 14.4 72.0 55836 13 ABD33347 Abd33347 Murine ca
c 713 14.4 72.0 92969 12 ACQ97202 Acq97202 Mouse can
c 714 14.4 72.0 95845 11 ACN44872 Acn44872 Mouse gen
c 715 14.4 72.0 105660 12 ADQ59446 3 Continuation (4 of
c 716 14.4 72.0 110000 6 ABQ69245 07 Continuation (8 of
c 717 14.4 72.0 110000 6 ABQ67197 06 Continuation (7 of
c 718 14.4 72.0 110000 12 ADQ34435 2 Continuation (3 of
c 719 14.4 72.0 110000 13 ABD32629 1 Continuation (2 of
c 720 14.4 72.0 110000 13 ABD32629 2 Continuation (3 of
c 721 14.4 72.0 117574 6 AAL45288 Aal45288 Human KCN
c 722 14.4 72.0 121160 12 ADQ97870 Adq97870 Human can
c 723 14.4 72.0 122336 13 ABD33303 Abd33303 Human can
c 724 14.4 72.0 134841 11 ACN45172 Acn45172 Mouse gen
c 725 14.4 72.0 138251 13 ADQ80324 Adq80324 Human PAC
c 726 14.4 72.0 178024 12 ADQ97721 Adq97721 Human can
c 727 14.4 72.0 179651 10 ADL13813 Adl13813 Osteoarth
c 728 14.4 72.0 179651 10 ADL13813 Adl13813 Osteoarth
c 729 14.4 72.0 191284 12 ADQ97957 Adq97957 Mouse can
c 730 14.4 72.0 247682 12 ADL08109 Adl08109 Human gen
c 731 14.4 72.0 299598 12 ADQ59380 Adq59380 Human can
c 732 14.4 72.0 304905 11 ADP75180 Adp75180 Human End
c 733 14.4 72.0 349980 5 AAH68532 Aah68532 C glutami
c 734 14.2 71.0 125 4 AAK24418 Aak24418 Human bra
c 735 14.2 71.0 173 12 ADG99042 Adg99042 Kidney di
c 736 14.2 71.0 179 2 AAT21179 Aat21179 Human gen
c 737 14.2 71.0 186 2 AAZ32055 Aaz32055 Human MET
c 738 14.2 71.0 186 5 AAC90312 Aac90312 M62458 cD
c 739 14.2 71.0 201 10 ADC92446 Adc92446 E. faeciu
c 740 14.2 71.0 219 3 AAC02572 Aac02572 Human sec
c 741 14.2 71.0 230 9 ACH44505 Ach44505 Human foe
c 742 14.2 71.0 251 5 AAH81857 Aah81857 Rat dlffe
c 743 14.2 71.0 262 7 ADE66050 Ade66050 Corn seed
c 744 14.2 71.0 270 6 ABS17969 Abs17969 Human gen
c 745 14.2 71.0 276 4 AAI20460 Aai20460 Probe #10
c 746 14.2 71.0 276 4 ABA65501 Aba65501 Human foe
c 747 14.2 71.0 276 4 AAI45666 Aai45666 Probe #14
c 748 14.2 71.0 276 4 ABA47606 Aba47606 Human bre
c 749 14.2 71.0 276 4 ABA32595 Aba32595 Probe #11
c 750 14.2 71.0 276 4 AAK39652 Aak39652 Human bon

ALIGNMENTS

RESULT 1
AAC86402
ID AAC86402 standard; mRNA; 20 BP.
XX
AC AAC86402;
XX
DT 28-FEB-2001 (first entry)
XX
DE Human bcl-2 mRNA nucleotides 2032-2051.
XX
KW Human; bcl-xL; bcl-2; apoptosis; antisense; cancer; allergic disease;
restenosis; fibrosis; psoriasis; ss.
XX
OS Homo sapiens.
XX
PN WO200066724-A2.
XX
PD 09-NOV-2000.
XX
PF 26-APR-2000; 2000WO-EP003708.
XX
PR 30-APR-1999; 99GB-00010119.
XX
PA (UYZU-) UNIV ZUERICH.
XX
PI Zangemeister-Wittke U, Luedke G, Huesken D;
WPI; 2001-015981/02.
XX
PT Antisense oligonucleotide derivatives directed against human bcl-xL mRNA
and capable of modulating biosynthesis of human bcl-xL proteins, useful
in treatment and diagnosis of hyperproliferative diseases.
XX
PS Disclosure; Page 5; 38pp; English.
XX
CC The present invention provides antisense nucleotides which hybridise to
the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins
are involved in apoptosis, and the antisense strands can be used to
inhibit them and possibly lead to cell death. The nucleic acids of the
invention can be used in the treatment of cancer, particularly
colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,
neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain
types of allergic disease
SQ Sequence 20 BP; 4 A; 4 C; 8 G; 0 T; 4 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCGUGGAGCCUU 20
|||||
DB 1 AACGGAGGCGUGGAGCCUU 20
RESULT 2
AAC86403/c
ID AAC86403 standard; RNA; 20 BP.
XX
AC AAC86403;
XX
DT 28-FEB-2001 (first entry)
XX
DE Human bcl-xL and bcl-2 mRNA antisense sequence #1.
XX
KW Human; bcl-xL; bcl-2; apoptosis; antisense; cancer; allergic disease;
restenosis; fibrosis; psoriasis; ss.
XX

OS Homo sapiens.
 PN WO200066724-A2.
 PD 09-NOV-2000.
 XX 26-APR-2000; 2000WO-EP003708.
 XX 30-APR-1999; 99GB-00010119.
 XX (UYZU-) UNIV ZUERICH.
 PA Zangemeister-Wittke U, Luedke G, Huesken D;
 PI WPI; 2001-015981/02.
 XX Antisense oligonucleotide derivatives directed against human bcl-xL mRNA
 PT and capable of modulating biosynthesis of human bcl-xL proteins, useful
 PT in treatment and diagnosis of hyperproliferative diseases.
 XX Claim 6; Page 29; 38pp; English.
 XX The present invention provides antisense nucleotides which hybridize to
 CC the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins
 CC are involved in apoptosis, and the antisense strands can be used to
 CC inhibit them and possibly lead to cell death. The nucleic acids of the
 CC invention can be used in the treatment of cancer, particularly
 CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,
 CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain
 CC types of allergic disease
 XX Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 80.0%; Pred. No. 10;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACGGAGGCTGGGATGCTT 1
 DB 20 AACGGAGGCTGGGATGCTT 1
 RESULT 3
 AD005981
 ID AD005981 standard; cDNA; 599 BP.
 XX AC AD005981;
 XX 15-JUL-2004 (first entry)
 XX Truncated human anti-apoptotic protein BCL-2 (deltaBCL-2) encoding cDNA.
 DE Autoimmune disease; pro-apoptotic protein; BAX; autoantigen; E3-GP19K;
 KW deltaBCL-2; type I diabetes; immunosuppressive; antidiabetic;
 KW gene therapy; gene; human; ss.
 XX Homo sapiens.
 OS WO2004034966-A2.
 PN 29-APR-2004.
 PD 06-AUG-2003; 2003WO-US024625.
 XX 06-AUG-2002; 2002US-0401652P.
 XX (UYLO-) UNIV LOMA LINDA.
 PA Escher AP, Li F;
 XX WPI; 2004-348318/32.
 XX New substance useful for treating or preventing an autoimmune disease
 PT comprises a polynucleotide construct comprising a sequence encoding the
 pro-apoptotic protein BAX and autoantigen for the autoimmune disease.
 Example 1; SEQ ID NO 3; 24pp; English.
 The invention relates to a substance for preventing, delaying the onset
 of, or treating one or more autoimmune disease, comprising a
 polynucleotide construct comprising a polynucleotide sequence encoding
 the pro-apoptotic protein BAX and one or more autoantigen for the
 autoimmune disease. The method involves: (a) selecting a patient who is
 susceptible to developing the autoimmune disease, who is developing an
 autoimmune disease, or who has the autoimmune disease; and (b)
 administering one or more dose of a polynucleotide construct encoding the
 pro-apoptotic protein BAX and one or more autoantigen for the autoimmune
 disease, the adenoviral protein E3-GP19K, deltaBCL-2, or a combination of
 these polynucleotide construct, where the autoimmune disease is type I
 diabetes. Selecting the patient comprises determining the presence of
 anti-insulin and/or anti-GAD autoantibodies, the presence of increasing
 hyperglycaemia, or the presence of glycosuria in the patient. The patient
 may also be selected by identifying the presence of a genetic
 predisposition to the autoimmune disease. After administration of the
 polynucleotide construct, the method further comprises monitoring the
 patient for the development of the autoimmune disease. The polynucleotide
 construct comprising a polynucleotide sequence which encodes the pro-
 apoptotic protein BAX and one or more autoantigen for the autoimmune
 disease, the adenoviral protein E3-GP19K, or deltaBCL-2, is useful for
 manufacturing of a medicament for preventing, delaying the onset of, or
 treating one or more autoimmune disease. The present sequence represents
 a human truncated anti-apoptotic protein BCL-2 (deltaBCL-2) encoding
 cDNA.
 XX Sequence 599 BP; 103 A; 171 C; 198 G; 127 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 20; DB 12; Length 599;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACGGAGGCTGGGATGCTT 20
 DB 439 AACGGAGGCTGGGATGCTT 458.
 RESULT 4
 ABT09345
 ID ABT09345 standard; DNA; 660 BP.
 XX AC ABT09345;
 XX 05-DEC-2002 (first entry)
 XX Phase-1 Rat CT gene SEQ ID No 433.
 DE Rat; toxicity study; rat toxic response gene; toxicological response;
 KW drug development; phase-1 rat CT gene; ds.
 XX Rattus sp.
 OS WO200266682-A2.
 PN 29-AUG-2002.
 PD 29-JAN-2002; 2002WO-US002935.
 XX 29-JAN-2001; 2001US-0264933P.
 PR 26-JUL-2001; 2001US-0308161P.
 XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 PA Farris G, Hicken SH, Farr SB;
 XX WPI; 2002-674961/72.
 XX Evaluating the toxicity of an agent, useful in drug development or in

PT determining toxicological responses to a new drug, by determining the
PT expression of rat toxicologically relevant genes in the test animal in
PT response to the test agent.
XX
XX
PS Disclosure; Page 213; 389pp; English.
XX
XX The invention relates to a method used for evaluating the toxicity of an
CC agent comprising determining the expression of a rat toxic response
CC gene(s) in the test animal in response to the agent. The method is useful
CC in drug development, particularly for conducting toxicity studies and
CC analysis before a new drug or compound is approved for human consumption
CC or use. The method is also useful in determining toxicological responses
CC to a new drug. This polynucleotide sequence represents a phase-1 rat CT
XX gene of the invention
XX
SQ Sequence 660 BP; 123 A; 189 C; 199 G; 147 T; 0 U; 2 Other;

Query Match 100.0%; Score 20; DB 6; Length 660;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
|||||:||||:||||:
Db 493 AACGGAGGCTGGATGCCTT 512

RESULT 5
ADH22708
ID ADH22708 standard; DNA; 661 BP.
XX
XX
AC ADH22708;
XX
DT 11-MAR-2004 (first entry)
XX
DE Partial DNA sequence of a rat kidney toxicity predictive gene (36).
XX
XX kidney toxicity; toxicology; predictive model; gene expression profile;
KW toxic damage; kidney tubule necrosis; acute renal failure; rat; ds.
XX
XX Rattus sp.
XX
XX WO2003100030-A2.
XX
PD 04-DEC-2003.
XX
PF 27-FEB-2003; 2003WO-US006196.
XX
XX 27-FEB-2002; 2002US-0361128P.
XX
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
XX Kier L, Nolan TD, Sankar U, Derbel M;
XX WPI; 2004-035137/03.
XX
PT Predicting kidney toxicity in an individual to an agent, useful for
PT predicting toxic responses to one or more agents comprising measuring the
PT expression of one or more kidney toxicity predictive genes.
XX
XX Claim 1; Page 323; 389pp; English.
XX
XX This invention relates to novel isolated kidney toxicity predictive genes
CC and methods of using such genes in the field of toxicology. Specifically,
CC it refers to novel genes that can be used for generating predictive
CC models, which in turn are useful for predicting the in vivo toxic
CC response to one or more agents. The present invention describes obtaining
CC a gene expression profile from a biological sample and using the
CC predictive model to determine whether an agent will induce kidney
CC toxicity in the individual. As such, it can be used to detect any toxic
CC effects that may be manifested as long lasting or chronic consequences
CC including irreversible toxicity or carcinogenesis. Furthermore, the
CC predictive genes can be considered as therapeutic targets for toxic
CC damage or to ameliorate specific disease conditions such as kidney tubule

CC necrosis or acute renal failure, as well as for additional screening
CC assays. This polynucleotide sequence is the partial gene sequence of a
CC rat kidney toxicity predictive gene of the invention.
XX
XX Sequence 661 BP; 123 A; 189 C; 200 G; 147 T; 0 U; 2 Other;

Query Match 100.0%; Score 20; DB 12; Length 661;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
|||||:||||:||||:
Db 494 AACGGAGGCTGGATGCCTT 513

RESULT 6
ADR91070
ID ADR91070 standard; cDNA; 661 BP.
XX
XX ADR91070;
XX
DT 16-DEC-2004 (first entry)
XX
XX Spleen necrosis predictive cDNA sequence, SEQ ID No 26.
DE altered expression; toxic response; spleen; toxicity; lymphoid; gene; ss.
XX
XX Unidentified.
XX
XX WO2004083402-A2.
PN
XX
PD 30-SEP-2004.
XX
XX 17-MAR-2004; 2004WO-US008371.
XX
XX 17-MAR-2003; 2003US-0455443P.
PR (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
XX Sankar U, Kier L, Derbel M, Nolan T;
XX WPI; 2004-691048/67.
XX
XX New composition comprises cDNAs useful for detecting altered expression
PT of genes in a toxic response of the spleen or for predicting toxic
PT responses to one or more agents including lymphoid tissue types or other
PT species.
XX
XX Claim 1; SEQ ID NO 26; 249pp; English.
XX
XX The invention relates to a novel composition comprising cDNAs for use in
CC detecting the altered expression of genes in a toxic response of the
CC spleen, where the cDNAs comprises 50-816 base pairs (ADR91045-ADR91348)
CC or their complete complements. The invention further comprises:
CC monitoring the treatment of compound toxicity in a sample; predicting the
CC spleen toxicity in an individual to an agent; predicting the spleen
CC toxicity of an agent using an in vitro system; a computer program product
CC for predicting spleen toxicity from an expression profile of nucleic
CC acids from a sample under test, comprising a computer readable medium
CC bearing an encrypted training data set, encrypted lists of genes selected
CC from the cDNAs, and a predictive model for causing a general purpose
CC computer to predict the spleen toxicity of the sample based upon the
CC training data set, the list of genes selected from the cDNAs, and the
CC expression profile of nucleic acids from the sample; and an integrated
CC system for predicting spleen toxicity, comprising means for measuring
CC gene expression profiles of spleen predictive genes from samples exposed
CC to the test agent and a computer system operably linked to the means that
CC is capable of implementing a predictive model. The composition comprising
CC cDNAs is useful for detecting altered expression of genes in a toxic
CC response of the spleen or for predicting toxic responses to one or more
CC agents including lymphoid tissue types or other species. The predictive
CC genes and models of the invention are useful for identifying and
CC evaluating various in vitro systems that can be used to accurately

CC predict in vivo toxicity. This polynucleotide sequence represents one of
 XX the genes predictive for spleen necrosis of the invention.

Sequence 661 BP; 123 A; 189 C; 200 G; 147 T; 0 U; 2 Other;
 Query Match 100.0%; Score 20; DB 13; Length 661;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
 |||||:||||:||||:
 Db 494 AACGGAGGCTGGGATGCTT 513

RESULT 7
 ABQ74483
 ID ABQ74483 standard; cDNA; 711 BP.

XX ABQ74483;

XX 21-OCT-2002 (first entry)

XX Mouse bcl-2 nucleotide sequence SEQ ID NO:1.

XX Mouse; DNA array sequence selection; gene; cDNA microarray; probe;
 XX immunology; tumour; cancer; cancer biology; immune cell; aging;
 XX drug testing; infection; autoimmune disease; arthritis; allergy; vaccine;
 XX ss.

XX Mus musculus.

XX WO200261135-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050618.

XX 19-DEC-2000; 2000US-00741238.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Lorenz M;

XX WPI; 2002-608530/55.

XX New composition comprising an array of cDNA probes immobilized on a solid
 XX support, useful for diagnostic and screening procedures involving
 XX immunologically-based sample materials, drug testing or monitoring
 XX disease progression.

XX Claim 1; Fig 3; 420pp; English.

XX The present invention describes a composition comprising an array of cDNA
 XX probes that are immobilised on a solid support, where the array comprises
 XX at least 10-20 probes having sequences selected from the 29 sequences of
 XX 192-4655 base pairs given in ABQ74483 to ABQ74511. Also described is a
 XX method for selecting DNA sequences for a non-redundant microarray,
 XX comprising: (a) providing sequence databases; (b) screening the databases
 XX for DNA sequences specific for a species and a tissue found in the
 XX species to generate a redundant sequence list; (c) removing redundant
 XX sequences from the list to generate a non-redundant cluster list; (d)
 XX categorising selected sequences from non-redundant cluster list into at
 XX least one module list; and (e) selecting the best representative clones
 XX based on the characteristics used to establish the parameters of the
 XX module list. The composition comprising the microarrays is useful in
 XX diagnostic and screening procedures involving immunologically-based
 XX sample materials. It is used in experiments and screens in innate and
 XX adaptive basic immunology, tumour immunology, cancer biology of immune
 XX cells, aging, drug testing, infection immunology, autoimmune diseases,
 XX arthritis, allergy, and vaccine development against these diseases. The
 XX composition and method may be used in monitoring the progression of a
 XX particular disease, in screening drug treatments for diseases, and in the
 XX construction of non-redundant DNA microarrays for different species

XX Sequence 711 BP; 127 A; 207 C; 225 G; 152 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 6; Length 711;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
 |||||:||||:||||:
 Db 565 AACGGAGGCTGGGATGCTT 584

RESULT 8
 ACN45149
 ID ACN45149 standard; cDNA; 711 BP.

XX ACN45149;

XX 18-NOV-2004 (first entry)

XX Mouse mRNA sequence mCT8968.

XX Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ds.

XX Mus musculus.

XX WO2003073826-A2.

XX 12-SEP-2003.

XX 28-FEB-2003; 2003WO-US006235.

XX 01-MAR-2002; 2002US-00087192.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW;

XX WPI; 2003-328604/31.

XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
 XX comprises a nucleotide sequence.

XX Claim 1; SEQ ID NO 1952; 0pp; English.

XX The present invention relates to novel DNA and protein sequences which
 XX are associated with carcinomas. The sequences are useful for: (i) for
 XX screening drug candidates; (ii) for screening of bioactive agent capable
 XX of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
 XX a bioactive agent capable of modulating the activity of CAP; (iv) for
 XX evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
 XX carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
 XX carcinoma; (viii) for neutralising the effect of CAP; (ix) as a biochip;
 XX (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
 XX determining Carcinoma Associated (CA) gene copy number. In addition, the
 XX CA genes are useful as DNA vaccines and the CAP are useful as markers of
 XX carcinoma including lymphoma. The present sequence is one such CA gene
 XX sequence. Note: This patent is an equivalent to basic patent
 XX US2002182586A1, for which no sequence data was published

XX Sequence 711 BP; 126 A; 208 C; 225 G; 152 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 11; Length 711;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
 |||||:||||:||||:
 Db 565 AACGGAGGCTGGGATGCTT 584

RESULT 9
 ABK90283

ID XX ABK90283 standard; DNA; 717 BP.
AC XX ABK90283;
XX
XX
XX 21-OCT-2002 (first entry)
XX
XX Bcl-2 antisense oligonucleotides associated DNA sequence #3.
DE XX
XX Antisense; ss; Bcl-2; cell proliferative disorder; cancer; CRE;
KW cAMP response element; bacterial infection; viral infection;
KW inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;
KW autoimmune disorder; parasitic infection; virucide; hyperplasia;
KW tumorigenesis; hepatitis B infection; human; gene.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 1..717
FT /*tag= a
FT /product= "Protein appearing as ABG31127"
FT /partial
FT /note= "No stop codon shown"
XX
XX WO200257480-A2.
XX
XX 25-JUL-2002.
XX
XX 22-JAN-2002; 2002WO-US001967.
XX
XX 22-JAN-2001; 2001US-0263244P.
XX
XX (GENT-) GENTA INC.
XX
XX Klem RE;
XX
XX WPI; 2002-590754/63.
DR P-PSDB; ABG31127.
XX
XX Hybrid oligomer comprises a cyclic AMP response element sequence and a
PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for
PT preventing or treating cell-proliferative disorders e.g., cancer.
XX
XX Disclosure; Page 71-72; 78pp; English.
XX
XX The invention relates to a hybrid oligomer comprising a cyclic AMP
CC response element (CRE) sequence and a sequence that hybridizes to the bcl
CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of
CC cancer cells in vitro, which comprises contacting the cancer cells with a
CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;
CC (2) treating or preventing cancer in a human, which comprises
CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE
CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid
CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a
CC carrier. The pharmaceutical composition of the invention is useful for
CC preventing or treating cell-proliferative disorders e.g., cancer,
CC hyperplasia or tumorigenesis and also bacterial infection, viral
CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,
CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and
CC bcl-2 antisense oligomer are also useful for preventing or treating
CC hepatitis B virus infection. The hybrid oligomers can also be used for
CC screening candidate transcription factors or other molecules e.g., gene
CC regulatory proteins or for diagnostic assays. The present sequence is a
CC Bcl-2 antisense oligonucleotide associated DNA sequence. Note: The
CC present sequence is included in the sequence listing but is not referred
CC to anywhere else in the specification
XX
XX Sequence 717 BP; 113 A; 237 C; 237 G; 130 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 6; Length 717;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGAGGCGGGAUGCCUU 20

Db 574 AACGAGGCTGGATGCCTT 593
|||||:||||:||||:||||:
RESULT 10
ABLS4167
ID ABL54167 standard; DNA; 717 BP.
XX
XX ABL54167;
XX AC
XX 12-JUL-2002 (first entry)
DT
XX Coding sequence.
DE
XX
XX B cell lymphoma/leukaemia-2; bcl-2; oncogene; antisense; lymphoma;
KW leukaemia; colon carcinoma; rectal carcinoma; pancreatic cancer;
KW breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;
KW hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;
KW testicular cancer; lung carcinoma; bladder carcinoma; melanoma;
KW head and neck cancer; brain cancer; cytostatic; human; gene therapy;
KW gene; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 1..717
FT /*tag= a
FT /partial
FT /note= "the CDS does not include a stop codon"
XX
XX WO200217852-A2.
XX
XX 07-MAR-2002.
XX
XX 23-AUG-2001; 2001WO-US026414.
XX
XX 25-AUG-2000; 2000US-0227970P.
PR 29-SEP-2000; 2000US-0237009P.
PR 10-NOV-2000; 2000US-00709170.
XX
XX (GENT-) GENTA INC.
XX
XX Warrel RP, Klem RE, Fingert H;
XX
XX WPI; 2002-371796/40.
DR P-PSDB; ABB75986.
XX
XX Treating or preventing cancer, tumors and carcinomas, comprises
PT administering B cell lymphoma/leukemia-2 antisense oligonucleotide at
PT high doses for short period for time with one or more cancer
PT therapeutics.
XX
XX Disclosure; Page 60; 64pp; English.
XX
XX The present invention is related to the use of a B cell
CC lymphoma/leukaemia-2 (bcl-2) antisense oligonucleotide, particularly
CC G3139 (see ABL54148), to treat and prevent bcl-2 related disorders.
CC Administration at high doses results in significant therapeutic
CC responses, including low toxicity, high tolerance and prolonged survival.
CC Administration at high doses for short periods of time (less than 14
CC days) also provides significant therapeutic responses in the treatment of
CC cancer. The bcl-2 antisense oligomer may also be used to increase the
CC sensitivity of a subject to cancer therapeutics, and in combination with
CC hormone treatment or gene therapy. Conditions that may be treated or
CC prevented include cancer of the haematopoietic system, skin, bone and
CC soft tissue, reproductive system, genitourinary system, breast, endocrine
CC system, brain, central nervous system, peripheral nervous system, kidney,
CC lung, respiratory system, thorax, gastrointestinal and alimentary canal,
CC lymph nodes, pancreas, hepatobiliary system, or cancer of unknown primary
CC site, non-Hodgkin's lymphoma, Hodgkin's lymphoma, leukaemia, colon
CC carcinoma, rectal carcinoma, pancreatic, breast, ovarian, prostate,
CC cervical, testicular, head and neck or brain cancer, renal cell
CC carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, lung

CC carcinoma, bladder carcinoma and melanoma (all claimed). Note: The
 CC present sequence is given in the Sequence Listing from the present
 CC invention but the Seq ID No. is not referred to within the specification
 XX
 SQ Sequence 717 BP; 113 A; 237 C; 237 G; 130 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 6; Length 717;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACGGAGGCTGGGATGCCCTT 593
 Db 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 11
 AAH45294
 ID AAH45294 standard; DNA; 720 BP.
 XX AAH45294;
 DT 10-SEP-2001 (first entry)
 DE DNA encoding human Bcl-2 protein mutant #1.
 XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; ds.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200142459-A1.
 XX 14-JUN-2001.
 XX 07-DEC-2000; 2000WO-JP008667.
 XX 09-DEC-1999; 99JP-00350427.
 XX (HISM) HISAMITSU PHARM CO LTD.
 PI Shibazaki F, Kuma H;
 DR WPI; 2001-381681/40.
 DR P-PSDB; AAG64036.
 XX New apoptosis inhibitors, useful for treating apoptosis related
 PT disorders.
 PS Claim 10; Page 36; 43pp; Japanese.
 CC The invention relates to an apoptosis inhibitor comprising the amino acid
 CC sequence of Bcl-2 protein in which at least one serine residue is
 CC substituted by alanine or aspartic acid. The protein has increased
 CC apoptosis inhibitory activity compared with the wild type Bcl-2 protein.
 CC The mutated Bcl-2 protein is useful in the treatment of disorders caused
 CC by apoptosis. The present sequence encodes a mutant Bcl-2 protein of the
 CC invention
 SQ Sequence 720 BP; 114 A; 237 C; 239 G; 130 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 720;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACGGAGGCTGGGATGCCCTT 593
 Db 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 12
 AAH45293
 ID AAH45293 standard; DNA; 720 BP.
 XX AAH45293;
 DT 10-SEP-2001 (first entry)
 DE DNA encoding human Bcl-2 protein mutant #4.
 XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; ds.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200142459-A1.
 XX 14-JUN-2001.
 XX 07-DEC-2000; 2000WO-JP008667.
 XX 09-DEC-1999; 99JP-00350427.
 XX (HISM) HISAMITSU PHARM CO LTD.

AC AAH45293;
 DT 10-SEP-2001 (first entry)
 DE Human Bcl-2 coding sequence.
 XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; ds.
 OS Homo sapiens.
 OS WO200142459-A1.
 XX 14-JUN-2001.
 XX 07-DEC-2000; 2000WO-JP008667.
 XX 09-DEC-1999; 99JP-00350427.
 XX (HISM) HISAMITSU PHARM CO LTD.
 PI Shibazaki F, Kuma H;
 DR WPI; 2001-381681/40.
 DR P-PSDB; AAG64035.
 XX New apoptosis inhibitors, useful for treating apoptosis related
 PT disorders.
 PS Disclosure; Page 35; 43pp; Japanese.
 CC The invention relates to an apoptosis inhibitor comprising the amino acid
 CC sequence of Bcl-2 protein in which at least one serine residue is
 CC substituted by alanine or aspartic acid. The protein has increased
 CC apoptosis inhibitory activity compared with the wild type Bcl-2 protein.
 CC The mutated Bcl-2 protein is useful in the treatment of disorders caused
 CC by apoptosis. The present sequence encodes the wild type human Bcl-2
 CC protein
 SQ Sequence 720 BP; 114 A; 237 C; 238 G; 131 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 720;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACGGAGGCTGGGATGCCCTT 593
 Db 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 13
 AAH45297
 ID AAH45297 standard; DNA; 720 BP.
 XX AAH45297;
 DT 10-SEP-2001 (first entry)
 DE DNA encoding human Bcl-2 protein mutant #4.
 XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; ds.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200142459-A1.
 XX 14-JUN-2001.
 XX 07-DEC-2000; 2000WO-JP008667.
 XX 09-DEC-1999; 99JP-00350427.
 XX (HISM) HISAMITSU PHARM CO LTD.

XX
PI Shibazaki F, Kuma H;
XX WPI; 2001-381681/40.
DR P-PSDB; AAG64039.
XX
PT New apoptosis inhibitors, useful for treating apoptosis related
PT disorders.
PS
PS Claim 13; Page 37; 43pp; Japanese.
XX
CC The invention relates to an apoptosis inhibitor comprising the amino acid
CC sequence of Bcl-2 protein in which at least one serine residue is
CC substituted by alanine or aspartic acid. The protein has increased
CC apoptosis inhibitory activity compared with the wild type Bcl-2 protein.
CC The mutated Bcl-2 protein is useful in the treatment of disorders caused
CC by apoptosis. The present sequence encodes a mutant Bcl-2 protein of the
CC invention
XX
SQ Sequence 720 BP; 114 A; 237 C; 238 G; 131 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 720;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCGUGGAGGCCUU 20
|||||||:|||||:|||||:
Db 574 AACGGAGGCTGGGATGCCTT 593
RESULT 14
AAH45296
ID AAH45296 standard; DNA; 720 BP.
AC AAH45296;
XX
XX 10-SEP-2001 (first entry)
XX
XX DNA encoding human Bcl-2 protein mutant #3.
XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; ds.
XX Homo sapiens.
XX Synthetic.
XX WO200142459-A1.
XX
XX 14-JUN-2001.
XX
XX 07-DEC-2000; 2000WO-JP008667.
XX
XX 09-DEC-1999; 99JP-00350427.
XX
XX (HISM) HISAMITSU PHARM CO LTD.
XX
XX Shibazaki F, Kuma H;
XX WPI; 2001-381681/40.
XX
XX New apoptosis inhibitors, useful for treating apoptosis related
XX disorders.
XX Claim 12; Page 37; 43pp; Japanese.
XX
CC The invention relates to an apoptosis inhibitor comprising the amino acid
CC sequence of Bcl-2 protein in which at least one serine residue is
CC substituted by alanine or aspartic acid. The protein has increased
CC apoptosis inhibitory activity compared with the wild type Bcl-2 protein.
CC The mutated Bcl-2 protein is useful in the treatment of disorders caused
CC by apoptosis. The present sequence encodes a mutant Bcl-2 protein of the
CC invention
XX
XX

SQ Sequence 720 BP; 113 A; 238 C; 238 G; 131 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 720;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCGUGGAGGCCUU 20
|||||||:|||||:|||||:
Db 574 AACGGAGGCTGGGATGCCTT 593
RESULT 15
AAH45295
ID AAH45295 standard; DNA; 720 BP.
XX
XX AAH45295;
AC
XX
XX 10-SEP-2001 (first entry)
XX
XX DNA encoding human Bcl-2 protein mutant #2.
XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; ds.
XX Homo sapiens.
XX Synthetic.
XX WO200142459-A1.
XX
XX 14-JUN-2001.
XX
XX 07-DEC-2000; 2000WO-JP008667.
XX
XX 09-DEC-1999; 99JP-00350427.
XX
XX (HISM) HISAMITSU PHARM CO LTD.
XX
XX Shibazaki F, Kuma H;
XX WPI; 2001-381681/40.
XX
XX New apoptosis inhibitors, useful for treating apoptosis related
XX disorders.
XX Claim 11; Page 36; 43pp; Japanese.
XX
CC The invention relates to an apoptosis inhibitor comprising the amino acid
CC sequence of Bcl-2 protein in which at least one serine residue is
CC substituted by alanine or aspartic acid. The protein has increased
CC apoptosis inhibitory activity compared with the wild type Bcl-2 protein.
CC The mutated Bcl-2 protein is useful in the treatment of disorders caused
CC by apoptosis. The present sequence encodes a mutant Bcl-2 protein of the
CC invention
XX
XX
SQ Sequence 720 BP; 113 A; 238 C; 239 G; 130 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 720;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCGUGGAGGCCUU 20
|||||||:|||||:|||||:
Db 574 AACGGAGGCTGGGATGCCTT 593
RESULT 16
ABA92889
ID ABA92889 standard; DNA; 720 BP.
XX
XX ABA92889;
AC
XX
XX 03-APR-2002 (first entry)
XX
XX Human D34A caspase-resistant form of Bcl-2 gene SEQ ID NO:1.
XX
XX

XX Human; D34A caspase-resistant Bcl-2; Bcl-2; mutant; vasotropic;
KW vascularisation; angiogenesis; tissue transplantation; grafting;
KW organ transplantation; gene; ss.
XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 1. .720
FT /*tag= a
FT /product= "D34A caspase-resistant form of Bcl-2"

XX WO200193880-A1.

XX 13-DEC-2001.

XX 05-JUN-2001; 2001KO-US018034.

XX 05-JUN-2000; 2000US-0208931P.

XX 30-MAR-2001; 2001US-027979P.

XX (UYVA) UNIV YALE.

XX Bothwell ALM, Pober JS, Schechner JS, Zheng L;

XX WPI; 2002-130568/17.

XX P-PSDB; ABB05227.

XX New synthetic composition comprising collagen, fibronectin and cells,
PT useful for forming cultured endothelial cells for tissue/organ
PT transplantation or grafting onto recipients with impaired
PT vascularization.

XX Example 2; Page 96-97; 99pp; English.

XX The present invention describes a synthetic composition, which comprises
CC collagen, fibronectin and at least one cell. Also described are: (1) a
CC construct prepared by a method (M1) comprising: (a) preparing a solution
CC comprising collagen and fibronectin; (b) suspending endothelial cells in
CC the solution of step (a), where the suspended endothelial cells comprise
CC a nucleic acid encoding a caspase-resistant Bcl-2 polypeptide; and (c)
CC polymerising the collagen within the solution of step (b) to form a three
CC dimensional gel; (2) a method (M2) of animal implantation comprising
CC implanting into an animal the construct produced by the method of (1);
CC (3) a method (M3) for forming endothelial cells into tubes within a
CC matrix; (4) a method (M4) of producing endothelial cell tubules in vivo;
CC (5) a method (M5) of promoting vascularisation in a tissue or an organ,
CC or in animal; (6) methods (M6) for identifying genes or gene products
CC involved in the process of vascularisation; (7) a method (M7) of
CC identifying an agent, which modulates vascularisation or vascular
CC remodeling; and (8) the endothelial cell tubules produced by the method
CC of (M4). The synthetic composition has vasotropic activity. The
CC composition is useful in methods for forming cultured endothelial cells
CC into tubes or forming cultured endothelial cells into tubes within a
CC three-dimensional gel. This is particularly useful in the grafting of
CC engineered skin onto recipients with impaired vascularisation or impaired
CC angiogenesis, or in all aspects of tissue and organ transplantation and
CC grafting. The present sequence encodes the human D34A caspase-resistant
CC form of Bcl-2, which is used in an example from the present invention

XX Sequence 720 BP; 113 A; 238 C; 238 G; 131 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 720;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGCCUU 20

DB 574 AACGGAGGCTGGGATGCTT 593

RESULT 17
ADF28075

ID ADF28075 standard; cDNA; 720 BP.

XX ADF28075;

XX 12-FEB-2004 (first entry)

XX Mutant Bcl-2 protein D34A encoding cDNA.

XX Bcl-2; endothelial cell; mutant; vascularisation; human; antidiabetic;
KW antiulcer; vulnery; cardiovascular; cell therapy; ss; gene.

XX Synthetic.

XX Key Location/Qualifiers

FH CDS 1. .720

FT /*tag= a

FT /product= "caspase-resistant Bcl-2"

XX WO2003087337-A2.

XX 23-OCT-2003.

XX 14-APR-2003; 2003WO-US011371.

XX 12-APR-2002; 2002US-0371677P.

XX (UYVA) UNIV YALE.

XX Bothwell ALM, Pober JS, Schechner JS;

XX WPI; 2003-833725/77.

XX P-PSDB; ADF28076.

XX New engineered human skin equivalent that becomes perfused in vivo after

XX engraftment on an immunodeficient animal, useful for treating conditions

XX involving impaired angiogenesis, e.g. diabetes, chronic leg ulcers or

XX wounds.

XX Example 2; SEQ ID NO 1; 144pp; English.

XX The invention relates to an engineered human skin equivalent, where the
CC skin equivalent becomes perfused in vivo after engraftment on an
CC immunodeficient animal. The method involves implanting onto a skin
CC surface wound of an animal a construct prepared by a method comprising:
CC preparing a solution comprising collagen and fibronectin; suspending
CC endothelial cells in the solution where the suspended endothelial cells
CC comprise a nucleic acid encoding a caspase-resistant Bcl-2 polypeptide;
CC adjusting the solution of step (b) to about pH 7.0-8.0; and warming the
CC solution of step (c) to about 25-40 degrees C to form a three-dimensional
CC gel. The method of endothelial cell transplantation promotes
CC vascularisation of human skin equivalents in vivo. Administration can be
CC orthotopic or subcutaneous. The engineered human skin equivalents and
CC methods are useful in treating diseases or conditions involving impaired
CC angiogenesis, such as diabetes, chronic leg ulcers, wounds,
CC cardiovascular disease or burns. The present sequence represents a cDNA
CC encoding a mutant form of Bcl-2 protein (Asp34Ala), which is a caspase-
CC resistant form of Bcl-2.

XX Sequence 720 BP; 113 A; 238 C; 238 G; 131 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 720;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGCCUU 20

DB 574 AACGGAGGCTGGGATGCTT 593

RESULT 18
ADR46370

ID ADR46370 standard; DNA; 720 BP.

XX

```
AC ADR46370;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human Bcl-2 protein coding sequence.
XX
KW cytostatic; immunotoxin; cancer; mitochondrial malate dehydrogenase;
XX enzyme; human; MDH; ds; gene; Bcl-2.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..720
FT /*tag= a
FT /*product= "Bcl-2"
XX
PN WO2004070012-A2.
XX
PD 19-AUG-2004.
XX
PF 02-FEB-2004; 2004WO-US002974.
XX
PR 02-FEB-2003; 2003US-00444191.
XX 03-FEB-2003; 2003US-0444191P.
XX 08-APR-2003; 2003US-0460855P.
XX
PA (PALO-) PALO ALTO INST MOLECULAR MEDICINE.
XX
PI Wright SC, Larrick JW, Nock SR, Wilson DS;
XX
DR WPI; 2004-604434/58.
XX P-PSDB; ADR46369.
XX
DR New compositions comprising proteins and encoding nucleic acids having a
PT DNA nuclease or cell killing activity and are operably linked to cancer
PT cell binding antibodies or growth factors, useful for treating cancer.
XX
PS Disclosure; SEQ ID NO 17; 225pp; English.
XX
CC The present invention relates to a composition comprising an isolated
CC amino acid sequence that comprises a portion of human mitochondrial
CC malate dehydrogenase protein (MDH), particularly the minimum activator of
CC DNA fragmentation and activator of DNA fragmentation sequences. The
CC composition is useful for treating cancer chosen from liver cancer,
CC gastric cancer, head cancer, neck cancer, lung cancer, breast cancer,
CC prostate cancer, cervical cancer, pancreatic cancer, colon cancer,
CC ovarian cancer, stomach cancer, esophageal cancer, mouth cancer, tongue
CC cancer, gum cancer, skin cancer, muscle cancer, heart cancer, bronchial
CC cancer, cartilage cancer, bone cancer, testis cancer, kidney cancer,
CC endometrium cancer, uterus cancer, bladder cancer, bone marrow cancer,
CC lymphoma cancer, spleen cancer, thymus cancer, thyroid cancer, brain
CC cancer, neuron cancer, gall bladder cancer, ocular cancer, joint cancer,
CC glioblastoma, mesothelioma, lymphoma, leukemia, melanoma, squamous cell
CC carcinoma, osteosarcoma, and Kaposi's sarcoma. The present sequence is a
CC coding sequence shown in the exemplification of the invention.
XX
SQ Sequence 720 BP; 114 A; 233 C; 241 G; 132 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 13; Length 720;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AACGGAGGCTGGGAGGCCUU 20
|||||:|||||:|:
Db 574 AACGGAGGCTGGGATGCTT 593
RESULT 19
ADSR4141
ID ADS74141 standard; cDNA; 720 BP.
XX
AC ADS74141;
XX
DT 04-JUN-1997 (first entry)
XX
DT 16-DEC-2004 (first entry)
XX
DE Human Bcl-2 alpha coding sequence.
XX
KW Human; Bcl-2 alpha; apoptosis; gene silencing; RNA interference; RNAi;
XX small interfering RNA; siRNA; cytostatic; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..720
FT /*tag= a
FT /*product= "Bcl-2 alpha"
XX
PN WO2004083240-A2.
XX
PD 30-SEP-2004.
XX
PF 17-MAR-2004; 2004WO-GB001128.
XX 18-MAR-2003; 2003GB-00006148.
XX
PR (MILN/) MILNER J.
XX
PI Milner J;
XX
DR WPI; 2004-691020/67.
XX P-PSDB; ADS74140.
XX GENBANK; NM_000633.
XX
DR Regulating apoptosis to treat e.g. cancer comprises introducing into a
PT cell an RNA construct that is homologous to mRNA within the cell, the
PT mRNA including genetic information of a gene element involved in the
PT regulation of apoptosis.
XX
PS Claim 4; Fig 6a; 38pp; English.
XX
CC The present sequence is the coding sequence for Bcl-2 alpha. A claimed
CC method of regulating apoptosis comprises introducing into a cell an RNA
CC construct comprising a nucleotide sequence which is homologous to mRNA
CC within the cell, where the mRNA includes genetic information of a gene
CC element involved in the regulation of apoptosis. The gene element
CC preferably comprises a nucleic acid molecule selected from: (i) a nucleic
CC acid molecule represented by Bcl-2 alpha, Bcl-2 beta or Bcl-XL mRNA or
CC its functional fragment; (ii) a nucleic acid molecule which hybridises to
CC any of the nucleic acid sequences in (i) and which has siRNA activity; or
CC (iii) a nucleic acid molecule which is degenerate in the genetic code to
CC the sequences of (i) and/or (ii). An siRNA construct comprising a
CC nucleotide sequence that is homologous to a part or fragment of Bcl-2 or
CC Bcl-XL, especially nucleotides 354-372 of Bcl-2 mRNA or nucleotides 347-
CC 366 of Bcl-XL mRNA, is also claimed. The siRNA is used in the regulation
CC of apoptosis in a cell. Uses of an RNA construct as a medicament to
CC induce apoptosis, for the treatment of colorectal cancer or for the
CC treatment of viral induced cancer are claimed.
XX
SQ Sequence 720 BP; 114 A; 233 C; 241 G; 132 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 13; Length 720;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AACGGAGGCTGGGAGGCCUU 20
|||||:|||||:|:
Db 574 AACGGAGGCTGGGATGCTT 593
RESULT 20
AAT33694
ID AAT33694 standard; cDNA; 760 BP.
XX
AC AAT33694;
XX
DT 04-JUN-1997 (first entry)
XX
```


PR 08-APR-1999; 99JP-00101888.
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 DR WPI; 2001-065575/08.
 DR P-PSDB; AAB50537.
 XX
 PT Screening of an apoptosis inhibitor or promoter which can be used as a
 PT drug and a diagnostic agent for various diseases caused by apoptosis
 PT inhibition or apoptosis promotion.
 XX
 PS Claim 15; Page 12-13; 22pp; Japanese.
 XX
 CC The present invention describes a method for screening for an apoptosis
 CC inhibitor or an apoptosis promoter in which VDAC-liposome, an index
 CC substance which can pass VDAC and a sample are incubated and the change
 CC in the concentration of the index substance during the incubation is
 CC detected to judge the presence of apoptosis inhibition or apoptosis
 CC promotion. The apoptosis inhibitor or the apoptosis promoter can be used
 CC as a drug and a diagnostic agent for various diseases caused by apoptosis
 CC inhibition or apoptosis promotion. The present sequence encodes the human
 CC Bcl-2 protein, which is an apoptosis inhibitor used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 771 BP; 124 A; 250 C; 251 G; 146 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 771;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACGGAGGCGGGAUGCCUU 20
 DB 605 AACGGAGGCTGGGATGCTT 624
 |||||:||||:||||:||||:
 RESULT 23
 ADO70418
 ID ADO70418 standard; cDNA; 931 BP.
 XX
 AC ADO70418;
 XX
 DT 26-AUG-2004 (first entry)
 DE Human Bcl-2 cDNA.
 XX
 KW Human; Bcl-2; Gene; ss; infection; inflammation; tumour formation;
 KW cancer; antibacterial; antiinflammatory; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO2004046327-A2.
 XX
 PD 03-JUN-2004.
 XX
 PF 14-NOV-2003; 2003WO-US036614.
 XX
 PR 14-NOV-2002; 2002US-0426269P.
 XX
 PA (GENT-) GENTA SALUS LLC.
 XX
 PI Chen Z, Ruffner DE, Prakash R, Koehn R;
 XX WPI; 2004-420620/39.
 DR
 CC New isolated oligonucleotide targeted to Bcl-2, useful for inhibiting
 CC expression of Bcl-2 in a cell, tissue, or organism, or for treating
 CC conditions susceptible to modulation of Bcl-2 expression in an organism.
 XX
 PS Disclosure; SEQ ID NO 18; 49pp; English.
 XX
 CC The invention relates to oligonucleotides that hybridise to a human Bcl-2
 CC polynucleotide. The invention also relates to a method for inhibiting
 CC expression of Bcl-2 in a cell, tissue, or organism, or for treating
 CC conditions susceptible to modulation of Bcl-2 expression in an organism.
 CC
 CC expression of Bcl-2, a method for detecting a nucleic acid encoding Bcl-2

CC and a method of treating a condition susceptible to modulation of Bcl-2
 CC expression. Inhibiting expression of Bcl-2 comprises administering an
 CC oligonucleotide of the invention to a cell, tissue or organism. Detecting
 CC a nucleic acid encoding Bcl-2 comprises hybridising the oligonucleotide
 CC to the nucleic acid encoding Bcl-2. The oligonucleotide further comprises
 CC a detectable label. Treating a condition susceptible to modulation of Bcl
 CC -2 expression in an organism comprises administering a composition
 CC comprising an oligonucleotide of the invention to the organism. The
 CC oligonucleotides can be incorporated in a pharmaceutical composition and
 CC can be used for inhibiting the expression of Bcl-2 in a cell, tissue or
 CC organism, for treating conditions susceptible to modulation of Bcl-2
 CC expression in an organism or for detecting a nucleic acid encoding Bcl-2.
 CC The compounds are useful for preventing or delaying infection,
 CC inflammation or tumour formation. This sequence represents human Bcl-2
 CC cDNA of the invention.
 XX
 SQ Sequence 931 BP; 191 A; 288 C; 281 G; 171 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 12; Length 931;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACGGAGGCGGGAUGCCUU 20
 DB 623 AACGGAGGCTGGGATGCTT 642
 |||||:||||:||||:||||:
 RESULT 24
 ADO70435
 ID ADO70435 standard; cDNA; 931 BP.
 XX
 AC ADO70435;
 XX
 DT 26-AUG-2004 (first entry)
 DE Human Bcl-2 variant cDNA.
 XX
 KW Human; Bcl-2; Gene; ss; infection; inflammation; tumour formation;
 KW cancer; antibacterial; antiinflammatory; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO2004046327-A2.
 XX
 PD 03-JUN-2004.
 XX
 PF 14-NOV-2003; 2003WO-US036614.
 XX
 PR 14-NOV-2002; 2002US-0426269P.
 XX
 PA (GENT-) GENTA SALUS LLC.
 XX
 PI Chen Z, Ruffner DE, Prakash R, Koehn R;
 XX WPI; 2004-420620/39.
 DR
 CC New isolated oligonucleotide targeted to Bcl-2, useful for inhibiting
 CC expression of Bcl-2 in a cell, tissue, or organism, or for treating
 CC conditions susceptible to modulation of Bcl-2 expression in an organism.
 XX
 PS Disclosure; SEQ ID NO 35; 49pp; English.
 XX
 CC The invention relates to oligonucleotides that hybridise to a human Bcl-2
 CC polynucleotide. The invention also relates to a method for inhibiting
 CC expression of Bcl-2, a method for detecting a nucleic acid encoding Bcl-2
 CC and a method of treating a condition susceptible to modulation of Bcl-2
 CC expression. Inhibiting expression of Bcl-2 comprises administering an
 CC oligonucleotide of the invention to a cell, tissue or organism. Detecting
 CC a nucleic acid encoding Bcl-2 comprises hybridising the oligonucleotide
 CC to the nucleic acid encoding Bcl-2. The oligonucleotide further comprises
 CC a detectable label. Treating a condition susceptible to modulation of Bcl
 CC -2 expression in an organism comprises administering a composition
 CC comprising an oligonucleotide of the invention to the organism. The

the compounds are useful for preventing or delaying infection, inflammation or tumour formation. This sequence represents human Bcl-2 variant cDNA of the invention.

Query Match	100.0%;	Score 20;	DB 2;	Length 953;
Best Local Similarity	80.0%;	Pred. No. 12;		
Matches 16:	Conservative 4;	Mismatches	0;	Indels 0;
				Gaps 0;

Qy 1 AACGAGGCUGGGAUGCCUU 20
638 AACGAGGCTGGGATGCCTT 657

RESULT 26
ADB58219

AC ADB58219:

DT 04-DEC-2003 (first entry)

Toxicity-related gene, SEO ID 3245.

Toxic; toxin; gene expression profile; hepatotoxicity; liver; drug screening; toxicity assay; ds.

Unidentified.

XX
PN
W02003064624-A2

XX

XX
FD-5007-BUY-10

PF 31-JAN-2003; 2003WO-US003194.

PR 31-JAN-2002; 2002US-00060087.

PR 15-MAR-2002; 2002US-0364045P.
PR 15-MAR-2002; 2002US-0364055P.

PR 30-DEC-2002; 2002US-043

XX
PA
(GENE-) GENE LOGIC INC

FT MEINUTICK D, FOLGET
XX

DR WPI; 2003-689530/65.

Sequence 1179 BP; 295 A; 316 C; 306 G; 262 T; 0 U; 0 Other; 22

Query Match 100.0%; Score 20; DB 10; Length 1179;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AACGGAGGCGUGGAUGCCUU 20
|||||||:::|||||:
Db 799 AACGGAGGCTGGGTGCCTT 818

RESULT 27
ADB52744
ID ADB52744 standard; DNA, 1179 BP.
XX XX
AC ADB52744;
XX XX
DT 04-DEC-2003 (first entry)
XX XX
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3286.
XX XX
KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
KW primary rat hepatocyte toxicity modelling; gene; ds.
XX XX
OS Rattus norvegicus.
XX XX
FN WO2003065993-A2.
XX XX
PD 14-AUG-2003.
XX XX
PF 04-FEB-2003; 2003WO-US003482.
XX XX
PR 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 19-APR-2002; 2002US-0373602P.
PR 22-APR-2002; 2002US-0374139P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.
PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378665P.
PR 09-JUL-2002; 2002US-0394230P.
PR 09-JUL-2002; 2002US-0394253P.
PR 08-SEP-2002; 2002US-0407688P.
PR 28-JAN-2003; 2003US-0442900P.
XX XX
PA (GENE-) GENE LOGIC INC.
XX XX
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI Elashoff M;
XX XX
DR WPI; 2003-731472/69.
XX XX
PT Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT mean values.

Claim 44; SEQ ID NO 3286; 874bp; English.

The present invention describes a method for determining whether a
compound induces a toxic effect on a tissue or cell. The method comprises
preparing a gene expression profile of a tissue or cell sample exposed to
the compound, and comparing the gene expression profile to a database
comprising data or information on the Tox mean and non-Tox mean value.
The method is useful for predicting or identifying at least one toxic
effect, particularly hepatotoxicity, of a test or unknown compound. The
genes listed in the specification are useful as diagnostic or toxicity
markers for the prediction or identification of the physiological state

of tissue or cell sample that has been exposed to a compound, or to
identify or predict the toxic effects of a compound or an agent. These
may also be used as markers for monitoring toxicity progression or for
drug screening. The present sequence represents a primary rat hepatocyte
toxicity modelling related gene sequence from the present invention.

Sequence 1179 BP; 295 A; 316 C; 306 G; 262 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 1179;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AACGGAGGCGUGGAUGCCUU 20
|||||||:::|||||:
Db 799 AACGGAGGCTGGGTGCCTT 818

RESULT 28
ADI62930
ID ADI62930 standard; cDNA; 2704 BP.
XX XX
AC ADI62930;
XX XX
DT 22-APR-2004 (first entry)
XX XX
DE Human apoptosis-associated cDNA SEQ ID 373.
XX XX
KW apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;
KW antirheumatic; antiarthritic; dermatological; antiinflammatory;
KW hepatotropic; viricide; nootropic; anticonvulsant; antiparkinsonian;
KW vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;
KW autoimmune disease; degenerative disease; viral infection; leukaemia;
KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;
KW lupus; hepatitis; influenza viruses; Alzheimer's disease;
KW Huntington's disease; Parkinson's diseases; reperfusion injury; stroke;
KW alcoholic liver disease; human; gene; ss.
XX XX
OS Homo sapiens.
XX XX
FN WO2003058021-A2.
XX XX
PD 17-JUL-2003.
XX XX
PF 13-JAN-2003; 2003WO-EP000270.
XX XX
PR 11-JAN-2002; 2002DE-01000856.
XX XX
PA (XANT-) XANTOS BIOMEDICINE AG.
XX XX
PI Koenig-Hoffman K, Kazinski M, Schaefer R, Kesper B;
XX XX
DR WPI; 2003-542134/51.
XX XX
PT New nucleic acids involved in apoptosis, useful for diagnosis and
PT treatment of e.g. tumors and degenerative disease, also related proteins,
PT antibodies and modulators.

Claim 1b; SEQ ID NO 373; 517pp; German.

This invention describes novel nucleic acid molecules that are associated
with apoptosis and encode a polypeptide and are derived from a normalised
gene library (embryonic or liver) or clone collections, and the extent of
apoptosis measured by cell death detection assay or the CPRG assay
(measuring loss of membrane integrity). The products of the invention
have cytotstatic, neuroprotective, immunosuppressive, antirheumatic,
antiarthritic, dermatological, antiinflammatory, hepatotropic, virucide,
cerebroprotective and antialcoholic activity and can be used for gene
therapy. The polynucleotides also related vectors, hosts (or their
extracts), encoded polypeptide (or their receptors) and/or agents that
inhibit their activity (including antisense sequences) are used for
treatment or prevention of tumours, autoimmune or degenerative diseases
and viral infections, specifically leukaemia carcinoma, sarcoma.

CC multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection
 CC with hepatitis or influenza viruses, Alzheimer's, Huntington's or
 CC Parkinson's diseases, reperfusion injury, stroke and alcoholic liver
 CC disease. Detection of the polynucleotides and derived polypeptides can
 CC also be used for diagnosis of these diseases. This sequence encodes an
 CC apoptosis-associated protein described in the disclosure of the
 CC invention.

XX
 SQ Sequence 2704 BP; 694 A; 660 C; 728 G; 622 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 10; Length 2704;
 Best Local Similarity 80.0%; Pred. No. 13;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGAGGCGGCGGAGCCUU 20
 |||||:||||:||||:||||:
 Db 963 AACGAGGCTGGGATGCTT 982

RESULT 29
 ABQ78540
 ID ABQ78540 standard; DNA; 5085 BP.
 AC ABQ78540;
 XX
 DT 25-NOV-2002 (first entry)
 XX
 DE Nucleotide sequence of human bcl-2.
 XX
 KW Antisense oligonucleotide; B cell lymphoma/leukemia-2 gene; bcl-2 gene;
 KW cancer; lymphoma; leukemia; chemotherapeutic agent; bone marrow purging;
 KW autoimmune disease; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1458..2178
 FT /*tag= a
 FT /product= "bcl-2"
 XX
 PN US6414134-B1.
 XX
 PD 02-JUL-2002.
 XX
 PF 28-NOV-2000; 2000US-00724426.
 XX
 PR 22-DEC-1988; 88US-00288692.
 PR 21-FEB-1992; 92US-00840716.
 PR 20-SEP-1993; 93US-00124256.
 PR 05-JUN-1995; 95US-00465485.
 PR 18-MAY-1998; 98US-00080285.
 PR 17-AUG-1999; 99US-00375514.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Reed JC;
 XX
 DR WPI; 2002-641579/59.
 DR P-PSDB; ABB78196.
 XX
 PT Novel antisense oligonucleotide complementary to B cell lymphoma/leukemia
 PT -2 mRNA, useful for inhibiting cancer cell growth, for treating
 PT autoimmune disorders, and for ex vivo bone marrow purging.
 XX
 PS Example 18; Col 33-38; 41pp; English.
 XX
 CC The present sequence encodes human B cell lymphoma/leukemia-2 (bcl-2).
 CC The specification describes antisense oligonucleotides complementary to B
 CC cell lymphoma/leukemia-2 (bcl-2) mRNA. The antisense oligonucleotide is
 CC useful for inhibiting cancer cell (lymphoma or leukemia cells) growth,
 CC for increasing the sensitivity of cancer cells to cancer chemotherapeutic
 CC agents, or for inducing cancer cell death alone or in combination with
 CC any one or more cancer chemotherapeutic agents. It is also useful for

CC reducing the bcl-2 gene expression or impairing bcl-2 protein function,
 CC for ex vivo bone marrow purging, for removing residual malignant cells
 CC from the bone marrow, for inhibiting cancer of neoplastic cell growth,
 CC and for treating autoimmune disease

XX
 SQ Sequence 5085 BP; 1262 A; 1224 C; 1286 G; 1313 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 6; Length 5085;
 Best Local Similarity 80.0%; Pred. No. 14;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGAGGCGGCGGAGCCUU 20
 |||||:||||:||||:||||:
 Db 2031 AACGAGGCTGGGATGCTT 2050

RESULT 30
 AAQ54631
 ID AAQ54631 standard; cDNA to mRNA; 5086 BP.
 XX
 AC AAQ54631;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-JUN-1994 (first entry)
 XX
 DE Human oncogene bcl-2 coding sequence.
 XX
 KW Cell death; senescence; programmed cell death; ced-9;
 KW myocardial infarction; stroke; brain injury; neurodegenerative disease;
 KW muscular degenerative disease; ageing; hypoxia; ischaemia; toxemia;
 KW infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2; oncogene;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1459..2178
 FT /*tag= a
 FT /product= "Bcl-2."
 XX
 PN WO9325603-A1.
 XX
 PD 23-DEC-1993.
 XX
 PF 14-JUN-1993; 93WO-US005651.
 XX
 PR 12-JUN-1992; 92US-00898933.
 PR 10-AUG-1992; 92US-00927681.
 XX
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 PI Horvitz HR, Hengartner M;
 XX
 DR WPI; 1994-007540/01.
 DR P-PSDB; AAR47344.
 XX
 PT Caenorhabditis elegans cell death-protective gene - used to develop
 PT agents for preventing cell death or for reducing population of cells.
 XX
 PS Disclosure; Page 61-64; 112pp; English.
 XX
 CC The protein product of the human oncogene bcl-2 was found to have a
 CC similar sequence to the ced-9 protein, ced-9 is essential for C. elegans
 CC development and apparently functions by protecting cells during
 CC development from programmed cell death. ced-9 was shown to function by
 CC antagonising the activities of cell death genes ced-3 and ced-4. The ced-
 CC 9 gene can be used for developing agents for treating a condition
 CC characterised by increased cell death such as myocardial infarction,
 CC stroke, traumatic brain injury, neurodegenerative disease, muscular
 CC degenerative disease, ageing, hypoxia, ischaemia, toxemia, infection or
 CC hair loss. It can also be used for reducing a population of cells in the
 CC treatment of neoplastic growth cancerous tissue, infected cells or
 CC autoreactive immune cells. (Updated on 25-MAR-2003 to correct PN field.)

```
XX SQ Sequence 5086 BP; 1262 A; 1222 C; 1288 G; 1314 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 5086;
Best Local Similarity 80.0%; Pred. NO. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGCCUU 20
Db 2032 AACGGAGCGCGGAGCCCTT 2051

RESULT 31
AAQ86661
ID AAQ86661 standard; DNA; 5086 BP.
XX AC AAQ86661;
XX DT 25-MAR-2003 (revised)
XX DT 27-SEP-1995 (first entry)
XX DE Human bcl-2 gene.
XX KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
XX KW Chemoresistance; ss.
XX OS Homo sapiens.
XX PN W09508350-A1.
XX PD 30-MAR-1995.
XX PF 20-SEP-1994; 94WO-US010725.
XX PR 20-SEP-1993; 93US-00124256.
XX PA (REED/) REED J C.
XX PI Reed JC;
XX DR WPI; 1995-139394/18.
XX PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment of human
XX PT solid tumours, esp. breast cancer.
XX PS Disclosure; Page 65-68; 108pp; English.
XX CC Reveal of chemoresistance of tumor cells by antisense-mediated
XX CC reduction of bcl1-2 expression was demonstrated using the oligonucleotide
XX CC given in AAQ86659. This is antisense to the first 6 codons of the bcl1-2
XX CC ORF. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 5086 BP; 1261 A; 1224 C; 1287 G; 1314 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 5086;
Best Local Similarity 80.0%; Pred. NO. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGCCUU 20
Db 2032 AACGGAGCGCGGAGCCCTT 2051

RESULT 32
AAQ75766
ID AAQ75766 standard; DNA; 5086 BP.
XX AC AAQ75766;
XX DT 22-JUL-1999 (first entry)
XX DE Human bcl2 proto-oncogene DNA.
XX
```

```
KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A; ss.
XX OS Homo sapiens.
XX PN W09845322-A2.
XX PD 15-OCT-1998.
XX PF 02-APR-1998; 98WO-IB000705.
XX PR 10-APR-1997; 97US-0043163P.
XX PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
XX PA (UTRO-) UNIV ROTTERDAM ERASMUS.
XX PA (UYUT-) RIJKSUNIV UTRECHT.
XX PI Van Leeuwen FW, Grosveld FG, Burbach JPH;
XX DR WPI; 1998-609901/51.
XX PT Diagnosing disease by detecting frameshift mutations in RNA or
XX PT corresponding protein mutations - used to diagnose cancer and
XX PT neurological diseases, particularly Alzheimer's disease, and also for
XX PT treatment and prevention with specific ribozymes or wild-type RNA.
XX PS Disclosure; Fig 15; 258pp; English.
XX CC This invention describes a novel method for the diagnosis of a disease
XX CC caused by, or associated with, an RNA molecule that has a frameshift
XX CC mutation. The method is used to diagnose age-related diseases, especially
XX CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
XX CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
XX CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
XX CC and many others listed) or susceptibility to these disorders. The method
XX CC allows a definitive diagnosis of Alzheimer's disease in living patients,
XX CC at an early stage. It is based on the observation that disease may be
XX CC caused by mutations in RNA rather than DNA. The invention describes the
XX CC use of neuronal system RNA molecules, specifically proteins including
XX CC beta-amyloid precursor protein (beta-APP), the microtubule associated
XX CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
XX CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
XX CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
XX CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
XX CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
XX CC protein-C (HMGP-C) and neuroendocrine specific protein A. This sequence
XX CC encodes the wild type and mutant protein fragments represented in
XX CC AAY21104-Y21263
XX SQ Sequence 5086 BP; 1262 A; 1224 C; 1287 G; 1313 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 5086;
Best Local Similarity 80.0%; Pred. NO. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGCCUU 20
Db 2032 AACGGAGCGCGGAGCCCTT 2051

RESULT 33
ABL54166
ID ABL54166 standard; DNA; 5086 BP.
XX AC ABL54166;
```

XX 12-JUL-2002 (first entry)
XX DNA sequence.
XX B cell lymphoma/leukaemia-2; bcl-2; oncogene; antisense; lymphoma;
KW leukaemia; colon carcinoma; rectal carcinoma; pancreatic cancer;
KW breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;
KW hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;
KW testicular cancer; lung carcinoma; bladder carcinoma; melanoma;
XX head and neck cancer; brain cancer; cytostatic; human; gene therapy; ds.
XX Homo sapiens.
XX WO200217852-A2.
XX 07-MAR-2002.
XX 23-AUG-2001; 2001WO-US026414.
XX 25-AUG-2000; 2000US-0227970P.
PR 29-SEP-2000; 2000US-0237009P.
PR 10-NOV-2000; 2000US-00709170.
XX (GENT-) GENTA INC.
XX Warrel RP, Klem FE, Fingert H;
XX WPI; 2002-371796/40.
XX Treating or preventing cancer, tumors and carcinomas, comprises
PT administering B cell lymphoma/leukemia-2 antisense oligonucleotide at
PT high doses for short period for time with one or more cancer
PT therapeutics.
XX Disclosure; Page 57-60; 64pp; English.
XX The present invention is related to the use of a B cell
CC lymphoma/leukaemia-2 (bcl-2) antisense oligonucleotide, particularly
CC G3139 (see ABL54148), to treat and prevent bcl-2 related disorders.
CC Administration at high doses results in significant therapeutic
CC responses, including low toxicity, high tolerance and prolonged survival.
CC Administration at high doses for short periods of time (less than 14
CC days) also provides significant therapeutic responses in the treatment of
CC cancer. The bcl-2 antisense oligomer may also be used to increase the
CC sensitivity of a subject to cancer therapeutics, and in combination with
CC hormone treatment or gene therapy. Conditions that may be treated or
CC prevented include cancer of the hematopoietic system, skin, bone and
CC soft tissue, reproductive system, genitourinary system, breast, endocrine
CC system, brain, central nervous system, peripheral nervous system, kidney,
CC lung, respiratory system, thorax, gastrointestinal and alimentary canal,
CC lymph nodes, pancreas, hepatobiliary system, or cancer of unknown primary
CC site, non-Hodgkin's lymphoma, Hodgkin's lymphoma, leukaemia, colon
CC carcinoma, rectal carcinoma, pancreatic, breast, ovarian, prostate,
CC cervical, testicular, head and neck or brain cancer, renal cell
CC carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, lung
CC carcinoma, bladder carcinoma and melanoma (all claimed). Note: The
CC present sequence is given in the Sequence Listing from the present
CC invention but the Seq ID No. is not referred to within the specification
XX
SQ Sequence 5086 BP; 1262 A; 1224 C; 1287 G; 1313 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGTGGGAUGCCUU 20
|||||||:|||||:
Db 2032 AACGGAGGTGGGATGCCTT 2051

RESULT 34
ABV75366

ID ABV75366 standard; DNA; 5086 BP.
XX AC ABV75366;
XX 07-MAR-2003 (first entry)
XX Human Bcl-2 polypeptide encoding DNA.
DE Caspase-9; TUCAN; cancer; biomarker; cIAP2; Apaf1; Bcl-2; Smac; human;
KW gene; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 1459..2178
FT /*tag= a
FT /note= "Bcl-2"
XX WO2002090931-A2.
XX 14-NOV-2002.
XX 07-MAY-2002; 2002WO-US014487.
XX 07-MAY-2001; 2001US-0289223P.
PR 12-FEB-2002; 2002US-0356934P.
XX (BURN-) BURNHAM INST.
XX Reed JC;
PI WPI; 2003-111999/10.
DR P-PSDB; ABB82742.
XX Determining a prognosis for survival for a cancer patient, useful for
PT determining if the patient is at risk for relapse, comprises measuring a
PT level of TUCAN in a sample from the patient, and comparing it to a
PT reference level.
XX Example; Page 147-150; 153pp; English.
XX The invention relates to determining a prognosis for survival for a
CC cancer patient. The method involves (a) measuring a level of a tumour up-
CC regulated CARD-containing antagonist of caspase-9 (TUCAN) in a neoplastic
CC cell-containing sample from the cancer patient; and (b) comparing the
CC level of TUCAN in the sample to a reference level of TUCAN, where a low
CC level of TUCAN in the sample correlates with increased survival of the
CC patient. Alternatively, the method involves measuring levels of TUCAN and
CC one or more biomarkers selected from the group of cIAP2, Apaf1, Bcl-2, or
CC Smac in a neoplastic cell-containing sample from the cancer patient. The
CC method is useful for determining if the patient is at risk for relapse,
CC or for determining a proper course of treatment for a patient with
CC cancer. The method is also useful for monitoring the effectiveness of a
CC course of treatment for a patient with cancer, e.g. colon cancer,
CC gastrointestinal cancer, breast cancer, ovarian cancer, lung cancer,
CC leukemia, CNS cancer, melanoma, prostate cancer, or renal cancer. The
CC present sequence represents a human Bcl-2 polypeptide encoding DNA
XX
SQ Sequence 5086 BP; 1262 A; 1224 C; 1287 G; 1313 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 5086;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGTGGGAUGCCUU 20
|||||||:|||||:
Db 2032 AACGGAGGTGGGATGCCTT 2051

RESULT 35
ACD28370
ID ACD28370 standard; cDNA; 5086 BP.
XX

```
AC ACD28370;
XX
XX 06-NOV-2003 (first entry)
XX
XX cDNA encoding human bcl-2.
XX
XX Cell death protective gene; ced-9; cerebroprotective; vulnery;
KW cardiant; nootropic; anticonvulsant; neuroprotective; antiparkinsonian;
KW viricide; anti-HIV; cytostatic; protozoacide; gene therapy;
KW antisenese therapy; programmed cell death; cell death disorder; aging;
KW stroke; traumatic brain injury; myocardial infarction;
KW Alzheimer's disease; degenerative disease; Huntington's disease;
KW amyotrophic lateral sclerosis; Parkinson's disease; infection; HIV;
KW cancer; neoplasia; pest control; human; gene; ss.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 1459..2178
XX /*tag= a
XX /product= "bcl-2"
XX
XX US2003064476-A1.
XX
XX 03-APR-2003.
XX
XX 06-NOV-2001; 2001US-009933420.
XX
XX 12-JUN-1992; 92US-00898933.
XX 10-AUG-1992; 92US-00927681.
XX 10-AUG-1994; 94US-00288295.
XX 19-FEB-1997; 97US-00801248.
XX 20-JAN-1999; 99US-00234186.
XX
XX (HORVITZ) HORVITZ H R.
XX (HENG) HENGARTNER M.
XX
XX Horvitz HR, Hengartner M;
XX
XX WPI; 2003-567186/53.
XX P-PSDB; ABU63582.
XX
XX New nucleic acid molecule for protecting cells against programmed cell
XX death or for preventing or treating diseases involving cell death, e.g.
XX stroke, traumatic brain injury, myocardial infarction or
XX neurodegenerative diseases.
XX
XX Example 2; Fig 7; 51pp; English.
XX
XX The invention describes an isolated nucleic acid comprising a fully
XX defined nucleotide sequence of 6560 base pairs (S1), as given in the
XX specification and encoding a polypeptide comprising a fully defined
XX sequence of 280 amino acids (S2), as given in the specification, where a
XX glutamic acid at position 74 is changed to lysine, and where the
XX nucleotide sequence encodes a loss-of-function mutant. The nucleic acid
XX is useful in protecting cells against programmed cell death by
XX antagonising the activities of genes that cause cell death. These genes
XX may be used for preventing or treating diseases or conditions involving
XX cell death, e.g. aging, stroke, traumatic brain injury, myocardial
XX infarction, degenerative diseases (including Huntington's disease,
XX amyotrophic lateral sclerosis, Alzheimer's disease or Parkinson's
XX disease), or viral and other types of infection (e.g. HIV). The genes may
XX also be used to increase cell death, for treating diseases, e.g. cancer
XX and neoplasia or in treating viral, parasitic and other infections and in
XX killing undesirable organisms, e.g. in pest control or in biological
XX containment applications. The nucleic acid can also be used in
XX identifying agents that affect the occurrence of cell death. This
XX sequence encodes human bcl-2, used in a comparison with Caenorhabditis
XX elegans cell protective protein ced-9
XX
XX Sequence 5086 BP; 1262 A; 1224 C; 1287 G; 1313 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 9; Length 5086;
```

```
Best Local Similarity 80.0%; Pred. No. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 AACGGAGCGUGGGAUGCCUU 20
DB 2032 AACGGAGCGTGGGATGCTT 2051
|||||:|||||:|||||:
RESULT 36
ADG87140
ID ADG87140 standard; DNA; 5086 BP.
XX
XX AC ADG87140;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Human Bcl-2 DNA.
XX
XX KW Cancer; TUCAN;
XX Tumour Up-regulated CARD-containing Antagonist of Caspase Nine;
XX Caspase-associated recruitment domain; melanoma; biomarker; apoptosis;
XX Gene; ds; prognosis; CARD; leukaemia; human; Bcl-2.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX CDS 1459..2178
XX FT /*tag= a
XX FT /product= "Bcl-2"
XX
XX PN US2003165887-A1.
XX
XX PD 04-SEP-2003.
XX
XX PF 07-MAY-2002; 2002US-00141618.
XX
XX PR 01-SEP-1999; 99US-00388221.
XX 07-MAY-2001; 2001US-0289233P.
XX 12-FEB-2002; 2002US-0356934P.
XX
XX PA (REED/) REED J C.
XX
XX PI Reed JC;
XX
XX WPI; 2004-020548/02.
XX P-PSDB; ADG87141.
XX
XX Diagnosing and determining prognosis for survival for cancer patient by
XX measuring levels of TUCAN (Tumor Up-regulated CARD-containing Antagonist
XX of Caspase Nine) for early detection of cancer and patients treated for
XX cancer.
XX
XX Disclosure; SEQ ID NO 11; 65pp; English.
XX
XX The invention relates to a method for determining a prognosis for
XX survival for a cancer patient by measuring levels of TUCAN (Tumour Up-
XX regulated CARD (caspase-associated recruitment domain)-containing
XX Antagonist of Caspase Nine). In the method the cancer is colon cancer,
XX gastrointestinal cancer, breast cancer, ovarian cancer, lung cancer,
XX leukaemia, CNS cancer, melanoma, prostate cancer and renal cancer. The
XX level of TUCAN nucleic acid can be measured. The patient is preferably in
XX the early stage of cancer. The level of TUCAN may be used to determine if
XX the patient is at risk of relapse or to determine a proper course of
XX treatment for the patient. In the method one of the biomarkers is
XX selected, or two or more biomarkers from the group consisting of cIAP2,
XX Apaf1, Bcl-2 and Smac. The methods are used for the early detection of
XX cancer, for monitoring patients being treated for advanced cancer and for
XX determining a prognosis for survival of a cancer patient. The use of
XX screening tests to detect cancers early leads to a more effective
XX treatment with fewer side effects. The invention plays a role in the
XX regulation of apoptosis. The present sequence is Bcl-2 DNA.
XX
XX Sequence 5086 BP; 1262 A; 1224 C; 1287 G; 1313 T; 0 U; 0 Other;
```

```

Query Match      100.0%; Score 20; DB 12; Length 5086;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGAGCCUU 20
        |||||:||||:||||:
Db      2032 AACGAGGCTGGGATGCCTT 2051

RESULT 37
AAD15284
ID      AAD15284 standard: DNA; 5087 BP.
XX
AC      AAD15284;
DT      15-NOV-2001 (first entry)
XX
DE      Human Bcl-2 protein DNA #1.
XX
KW      Human; Bcl-2 protein; cytostatic; lymphoma; cancer therapy; liposome;
KW      chronic lymphocytic leukaemia; plasma cell dyscrasia; cancer; pancreas;
KW      breast; liver; lung; brain; ovary; stomach; prostate; neck; oesophagus;
KW      testes; skin; head; kidney; colon; immune disorder; chromosome 18q21. ds.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      1459..2178
FT      /*tag= a
FT      /product= "Human Bcl-2 protein #1"
XX
XX      WO200160998-A2.
XX
XX      23-AUG-2001.
XX
XX      20-FEB-2001; 2001NO-US040159.
XX
XX      18-FEB-2000; 2000US-00506979.
XX
XX      (TEXA ) UNIV TEXAS SYSTEM.
XX
XX      Tari AM, Lopez-Barestein G, Gutierrez-Puente Y;
PI
DR      WPI; 2001-529911/38.
DR      P-PSDB; AAE08573.
XX
XX      Compositions comprising short antisense oligonucleotides and a lipid
XX      component, useful for treating Bcl-associated diseases, e.g. cancer.
XX
XX      Disclosure; Page 57-60; 63pp; English.
XX
XX      The invention relates to a liposomal composition of antisense
XX      oligonucleotides targeted to the translation initiation site of human
XX      Bcl-2 mRNA. The invention also relates to a method useful for treating
XX      Bcl-associated diseases like cancer such as follicular and nonfollicular
XX      lymphomas, chronic lymphocytic leukaemia and plasma cell dyscrasias;
XX      solid tumours like those associated with breast, prostate, liver,
XX      pancreas, lung, brain, ovary, testes, skin, head, neck, oesophagus,
XX      stomach, kidney and colon cancer; and immune disorders. The present DNA
XX      sequence encodes human Bcl-2 protein related to the invention. Human bcl-
XX      2 gene is located on chromosome 18q21
XX
XX      Sequence 5087 BP; 1262 A; 1224 C; 1287 G; 1313 T; 0 U; 1 Other;

Query Match      100.0%; Score 20; DB 5; Length 5087;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGAGCCUU 20
        |||||:||||:||||:
Db      2032 AACGAGGCTGGGATGCCTT 2051

RESULT 38
AAN81292
ID      AAN81292 standard; cDNA; 5105 BP.
XX
AC      AAN81292;
DT      17-DEC-1990 (first entry)
XX
DE      Sequence of bcl-2 cDNA corresp. to the 5.5 kb transcript encoding bcl-2-
DE      alpha.
XX
KW      B-cell neoplasm; diagnosis; follicular lymphomas; se.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      1459..2178
FT      /*tag= a
XX
XX      EP252685-A.
XX
XX      13-JAN-1988.
XX
XX      02-JUL-1987; 87EP-00305863.
XX
XX      09-JUL-1986; 86US-00883687.
XX
XX      (WIST-) WISTAR CORP.
XX
XX      Tsujimoto Y, Croce CW;
PI
DR      WPI; 1988-008633/02.
DR      P-PSDB; AAP80987.
XX
XX      Detection of B-cell neoplasms - by extn. of proteins or RNA from B-cells
XX      and quantitation using specific antibody or DNA probe.
XX
XX      Claim 8; Fig 2A-2D; 23pp; English.
XX
XX      A human bcl-2 gene substantially free of introns is claimed. Also claimed
XX      is a substantially pure preparation of a protein having an N-terminal end
XX      encoded by the first exon of the human bcl-2 gene wherein said protein is
XX      bcl-2-alpha having about 239 (AAP80987) or 205 (AAP80988) AA residues. B-
XX      cell neoplasms which are associated with t(14;18) chromosome
XX      translocations cause an increase in the expression of both mRNA and the
XX      protein prods. of the bcl-2 gene. This is used to detect B-cell neoplasms
XX      including follicular lymphomas as well as other lymphomas. Bacterial
XX      isolates available as ATCC 67147 and 67148 can be used to express gene
XX      prods. alpha (AAN81292) and beta (AAN91293) resp. in bacteria
XX
XX      Sequence 5105 BP; 1281 A; 1225 C; 1286 G; 1313 T; 0 U; 0 Other;

Query Match      100.0%; Score 20; DB 1; Length 5105;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGAGCCUU 20
        |||||:||||:||||:
Db      2032 AACGAGGCTGGGATGCCTT 2051

RESULT 39
ABV94126
ID      ABV94126 standard; cDNA; 6030 BP.
XX
AC      ABV94126;
XX
DT      08-JAN-2003 (first entry)
XX
DE      Breast carcinoma related nucleotide sequence SEQ ID NO:117.
XX
KW      Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;

```

KW ss.
 XX Homo sapiens.
 OS
 FN WO200246467-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 07-DEC-2001; 2001WO-IB002811.
 XX
 PR 08-DEC-2000; 2000US-0254090P.
 PR 07-DEC-2001; 2001US-00007926.
 XX
 PA (IPSO-) IPSOGEN.
 XX
 XX Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;
 PI WPI; 2002-619023/66.
 XX
 DR Novel polynucleotide library useful in molecular characterization of a
 XX carcinoma, comprising a pool of polynucleotide sequences or its
 PT sub-sequences which are either underexpressed or overexpressed in tumor
 PT cells.
 PT
 PS Claim 1; Page 185-187; 401pp; English.
 XX
 CC The present invention describes a polynucleotide library (I) useful in
 CC the molecular characterisation of a carcinoma, comprising a pool of
 CC polynucleotides or its subsequences which are either underexpressed or
 CC overexpressed in tumor cells, and correspond to any of the
 CC polynucleotide sequences chosen from the 468 sequences given in ABV94010
 CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for
 CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting
 CC (MI) differentially expressed polynucleotide sequences which are
 CC correlated with a cancer, involves obtaining a polynucleotide sample from
 CC a patient, and reacting the polynucleotide sample obtained with a probe
 CC immobilised on a solid support, where the probe comprises any combination
 CC of the polynucleotide sequences of (I) or its expression products encoded
 CC by polynucleotide sequences of (I), and detecting the reaction product.
 CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)
 CC is useful in molecular characterisation of a carcinoma. (I) and (II) are
 CC useful for the prognosis or diagnostic of tumour, in differentiating a
 CC normal cell from a cancer cell, detecting a hormone sensitive tumour
 CC cell, differentiating a tumour with lymph nodes from a tumour without
 CC lymph nodes, differentiating antineoplastic-sensitive tumours from
 CC antineoplastic-insensitive tumours, and classifying good and poor prognosis
 CC primary breast tumours. (I) is useful for large-scale molecular
 CC characterisation of breast cancer that help in prediction, prognosis and
 CC cancer treatment, and for detecting differentially expressed genes that
 CC correlated with a cancer
 XX
 SQ Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 6; Length 6030;
 Best Local Similarity 80.0%; Pred. No. 14;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACGGAGCGGCGGAGCCUU 20
 |||||:||||:||||:||||:
 Db 605 AACGGAGCGTGGGATGCCCTT 624
 RESULT 40
 ADE84951
 ID ADE84951 standard; DNA; 6030 BP.
 XX
 AC ADE84951;
 XX
 DT 03-APR-2003 (first entry)
 XX
 DE Human bcl-2 gene SEQ ID No 2.
 XX
 KW Anti-tumour; DNazyme; bcl-2 gene; tumour; malignant; chemotherapy;

KW radiation therapy; catalytic domain; enzyme; human; ds.
 XX
 OS Homo sapiens.
 XX
 FN WO200299090-A1.
 XX
 PD 12-DEC-2002.
 XX
 PF 07-JUN-2002; 2002WO-AU000739.
 XX
 PR 07-JUN-2001; 2001AU-00005527.
 PR
 XX (JOHJ) JOHNSON & JOHNSON RES PTY LTD.
 PA
 XX Sun L, Wang L, Turner RJ, Saravolac EG, Dass CR;
 PI WPI; 2003-140617/13.
 XX
 DR Novel DNazyme useful for treating tumors, and for enhancing the
 XX sensitivity of malignant or virus infected cells to therapy, comprises a
 PT catalytic domain and binding domain contiguous to the catalytic domain.
 PT
 PS Disclosure; Page 42-44; 67pp; English.
 XX
 CC The invention relates to a DNazyme which specifically cleaves mRNA
 CC transcribed from a member of the bcl-2 gene family. The DNazymes comprise
 CC a catalytic domain, binding domains contiguous with the 5' and 3' end of
 CC the catalytic domain, and therefore hybridise with, the two regions
 CC immediately flanking the purine residue of the cleavage site within the
 CC bcl-2 gene family mRNA, at which DNazyme-catalysed cleavage is desired. A
 CC pharmaceutical composition comprising a DNazyme of the invention is
 CC useful for treating tumours in a subject, and for enhancing the
 CC sensitivity of malignant or virus infected cells to therapy.
 CC The DNazymes are useful in diagnostics, therapeutics, to
 CC prophylaxis, research agents and in kits. The DNazymes are also useful
 CC for increasing the susceptibility of tumour cells to anti-tumour
 CC therapies such as chemotherapy and radiation therapy. This polynucleotide
 CC sequence represents a human bcl-2 gene of the invention
 XX
 SQ Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 8; Length 6030;
 Best Local Similarity 80.0%; Pred. No. 14;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACGGAGCGGCGGAGCCUU 20
 |||||:||||:||||:||||:
 Db 605 AACGGAGCGTGGGATGCCCTT 624
 RESULT 41
 ADE84951
 ID ADE84951 standard; DNA; 6030 BP.
 XX
 AC ADE84951;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Farnesyl transferase inhibitor modulated leukemia associated gene #170.
 XX
 KW ss; cytostatic; farnesyl transferase inhibitor; gene expression;
 KW quinolinone; leukemia; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2003038129-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 30-OCT-2002; 2002WO-US034784.
 XX
 PR 30-OCT-2001; 2001US-0338997P.
 PR 30-OCT-2001; 2001US-0340081P.

```

PR 30-OCT-2001; 2001US-0340938P.
PR 30-OCT-2001; 2001US-0341012P.
XX (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX Raponi M;
XX WPI; 2003-513497/48.
DR WPI; 2003-513497/48.
XX Determining whether a patient will respond to treatment with a farnesyl
PT transferase inhibitor, by analyzing the expression of gene that is
PT differentially modulated in the presence of the inhibitor.
PT Differentially modulated in the presence of the inhibitor.
XX Disclosure; SEQ ID NO 170; 346pp; English.
XX The invention relates to a method of determining whether a patient will
CC respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC analyzing the expression of gene that is differentially modulated in the
CC presence of an FTI. The method is useful for determining whether a
CC patient will respond to treatment with a FTI such as (B)-6-[amino(4-
CC chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
CC methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a
CC patient with leukemia with FTI if the analysis indicates that the patient
CC will respond. This sequence corresponds to a gene whose expression may be
CC modulated in the presence of FTI.
XX
SQ Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 10; Length 6030;
Best Local Similarity 80.0%; Pred. NO. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
DB 605 AACGGAGGCTGGGATCCTT 624
|||||:|||||:|||||:
RESULT 42
ADG32700
ID ADG32700 standard; DNA; 6030 BP.
XX
AC ADG32700;
XX
DT 26-FEB-2004 (first entry)
DE Human DNA differentially expressed in patients with SLE SeqID24.
XX
KW human; ds; autoimmune; chronic inflammatory disease; SLE;
KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;
KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;
KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;
KW diverticulitis; primary biliary sclerosis.
OS Homo sapiens.
XX
PN WO2003090694-A2.
XX
PD 06-NOV-2003.
XX
PF 24-APR-2003; 2003NO-US013015.
XX
PR 24-APR-2002; 2002US-00131827.
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgemuth J, Fry K, Woodward R, Ly N;
XX WPI; 2003-877243/31.
XX Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
PT colitis, psoriasis and asthma by detecting the expression level of one or
PT more genes.

```

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XX Claim 18; SEQ ID NO 24; 877pp; English.
XX This invention relates to novel methods for diagnosing and monitoring
CC autoimmune and chronic inflammatory diseases. Specifically, it refers to
CC the identification of genes that have a clinical utility as diagnostic
CC tools for the management of, in particular, patients with systemic lupus
CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the
CC present invention describes a method for determining the levels of
CC multiple differentially expressed genes of a patient, in a concerted
CC manner, in order to achieve an improved diagnostic assay with sensitivity
CC and specificity for the disease in question. As such, these genes are
CC useful for the diagnosis of various other inflammatory disorders
CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
CC ankylosing spondylitis, ulcerative colitis, primary sclerosing
CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.
CC This polynucleotide is a DNA sequence representing human mRNA that is
CC differentially expressed in patients with SLE, used in an exemplification
CC of the invention.
XX
SQ Sequence 6030 BP; 1666 A; 1246 C; 1388 G; 1730 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 10; Length 6030;
Best Local Similarity 80.0%; Pred. NO. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
DB 605 AACGGAGGCTGGGATCCTT 624
|||||:|||||:|||||:
RESULT 43
ADH28919
ID ADH28919 standard; DNA; 6030 BP.
XX
AC ADH28919;
XX
DT 11-MAR-2004 (first entry)
DE Human chronic myelogenous leukaemia (CML) gene marker #187.
XX
KW ds; chronic phase chronic myelogenous leukaemia; CP-CML;
KW blast crisis CML; BC-CML; human; chronic myelogenous leukaemia;
KW gene marker.
XX
OS Homo sapiens.
XX
PN US2003104426-A1.
XX
PD 05-JUN-2003.
XX
PF 14-JUN-2002; 2002US-00171581.
XX
PR 18-JUN-2001; 2001US-0298914P.
XX (LINS/) LINSLEY P S.
PA (MAOM/) MAO M.
PA (DAIH/) DAI H.
PA (HEXY/) HE Y.
PA (RADI/) RADICH J P.
XX
PI Linsley PS, Mao M, Dai H, He Y, Radich JP;
XX WPI; 2003-787046/74.
XX
PT Classifying cell sample as chronic phase chronic myelogenous leukemia or
PT blast crisis chronic myelogenous leukemia by detecting difference in
PT expression of genes corresponding to the markers such as X15415, U89436.
XX
PS Disclosure; SEQ ID NO 187; 31pp; English.
XX The invention relates to a method of classifying a cell sample as chronic
CC phase chronic myelogenous leukaemia (CP-CML) or blast crisis CML (BC-

```

CC CML). The method is useful for classifying a sample as CP-CML or BC-CML.
CC The present sequence represents a human chronic myelogenous leukaemia
CC (CML) gene marker used to distinguish blast crisis CML from chronic phase
CC CML.
XX
XX
SQ Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 6030;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
|||||:|||||:|||||:
Db 605 AACGGAGGCTGGGATGCCTT 624

RESULT 44
ADG89341
ID ADG89341 standard; DNA; 6030 BP.
XX
AC ADG89341;
XX
XX
DT 11-MAR-2004 (first entry)
DE Cancer detection method related gene #4.
XX
XX ds; cancer; gene expression;
KW estrogen receptor-positive invasive breast cancer.
XX
XX Homo sapiens.
OS
XX
XX WO2003078662-A1.
XX
XX 25-SEP-2003.
XX
XX
XX 12-MAR-2003; 2003WO-US007713.
XX
XX 13-MAR-2002; 2002US-0364890P.
PR
PR 18-SEP-2002; 2002US-0412049P.
XX
XX (GENO-) GENOMIC HEALTH INC.

PI Baker JB, Cronin MT, Kiefer MC, Shak S, Walker MG;
XX
XX WPI; 2003-767536/72.
XX
XX
XX Predicting clinical outcome for a patient diagnosed with cancer comprises
PT determining the expression level of one or more genes, and compared to
PT the amount found in a reference cancer tissue set.
XX
XX
XX Disclosure; SEQ ID NO 289; 198pp; English.

XX
XX The invention relates to a method of predicting clinical outcome for a
XX patient diagnosed with cancer by determining the expression level of one
XX or more genes, or their expression products, selected from p53BP2,
XX cathepsin B, cathepsin L, Ki67/MiB1, and thymidine kinase in a cancer
XX tissue obtained from the patient, normalized against control gene(s), and
XX compared to the amount found in a reference cancer tissue set. The
XX specification also discloses an array comprising polynucleotides
XX hybridizing to the following genes: FOXM1, PRAME, Bcl2, STK15, CEGP1, Ki-
XX 67, GSTM1, CA9, PR, BCC3, NME1, SURV, GATA3, TFR3, YB-1, DPYD, GSTM3,
XX RP56KB1, SRO, Chk1, ID1, EstR1, p27, CCNB1, XIAP, Chk2, CDC25B, IGFIR,
XX AK055699, P13KCA2A, TGF33, BAG1, CYP3A4, EPCAM, VEGFC, p52, hENT1, WTSP1,
XX HNF3A, NFKBp65, BRCA2, EGFR, TK1, VDR, Contig51037, pENT1, EPHX1, IFTA,
XX CDH1, HIF1, IGFBP3, CTSSB, Her2 and DIABLO, immobilized on a solid
XX surface. The methods are useful for predicting clinical outcome for a
XX patient diagnosed with cancer, classifying cancer, and predicting the
XX likelihood of long-term survival of a breast cancer patient, or a patient
XX diagnosed with invasive breast cancer or with estrogen receptor (ER)-
XX positive invasive breast cancer. This sequence corresponds to a gene
XX sequence whose expression is detected by the method of the invention.

XX Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 6030;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
|||||:|||||:|||||:
Db 605 AACGGAGGCTGGGATGCCTT 624

RESULT 45
ADI31689
ID ADI31689 standard; cDNA; 6030 BP.

XX AC ADI31689;
XX
XX
DT 17-JUN-2004 (first entry)
XX
XX Human cDNA #1015.

XX Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hyperesoinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antitumor;
KW osteopathic; antiarthritic; antirheumatic; antirheumatic; cytostatic.

XX Homo sapiens.

XX OS

XX PN US6607879-B1.

XX PD 19-AUG-2003.

XX PF 09-FEB-1998; 98US-00023655.

XX PR 09-FEB-1998; 98US-00023655.

XX (INCY-) INCYTE CORP.

XX PI Cocks BG, Stuart SG, Seilhamer JJ;

XX DR WPI; 2003-895307/82.

XX
XX A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.

XX Claim 1; SEQ ID NO 1015; 50pp; English.

XX The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hyperesoinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the

CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification but was obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 11; Length 6030;
 Best Local Similarity 80.0%; Pred. No. 14;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
 |||||:||||:||||:||||:
 Db 605 AACGGAGGCTGGGATGCCCTT 624

RESULT 46

ADL83240
 ID ADL83240 standard; cDNA; 6030 BP.

XX AC ADL83240;

XX DT 17-JUN-2004 (first entry)

XX DE Human PRO84722 cDNA, SEQ ID 442.

XX KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
 KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
 KW Gene Therapy; PRO; B cell related disorder; cancer;
 KW immune-mediated inflammatory disease; human; gene; ss.

XX OS Homo sapiens.

XX PN WO2004024097-A2.

XX PD 25-MAR-2004.

XX PF 15-SEP-2003; 2003WO-US029097.

XX PR 16-SEP-2002; 2002US-0411392P.

XX PA (GETH) GENENTECH INC.

XX PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
 PI Wu TD;

XX WPI; 2004-329389/30.

XX DR P-PSDB; ADL83241.

XX PT New PRO polypeptide, useful for diagnosing and treating a B cell related
 PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
 PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.

XX PS Claim 2; Fig 442; 695pp; English.

XX CC The present invention relates to PRO proteins and their coding sequences.
 CC The PRO proteins are useful for diagnosing and treating a B cell related
 CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
 CC antigen unresponsiveness, selective IgA deficiency, selective IgM
 CC deficiency, selective deficiency of IGH subclasses, immunodeficiency with
 CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
 CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
 CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
 CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
 CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
 CC medicament for treating a condition that is responsive to the PRO
 CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
 CC coding sequences are useful as hybridization probes in chromosome and
 CC gene mapping, in preparing PRO proteins, or in generating transgenic
 CC animals or knockout animals, which in turn are useful in the development
 CC and screening of therapeutically useful reagents.

XX SQ Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 6030;
 Best Local Similarity 80.0%; Pred. No. 14;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
 |||||:||||:||||:||||:
 Db 605 AACGGAGGCTGGGATGCCCTT 624

RESULT 47

AD019395
 ID AD019395 standard; cDNA; 6030 BP.

XX AC AD019395;

XX DT 12-AUG-2004 (first entry)

XX DE Human PRO polynucleotide #163.

XX KW Human; PRO; gene; ss; immune related disorder;
 KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
 KW juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome;
 KW vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
 KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
 KW renal disease; demyelinating disease; central nervous system;
 KW peripheral nervous system; demyelinating polyneuropathy;
 KW Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.

XX OS Homo sapiens.

XX PN WO2004043361-A2.

XX PD 27-MAY-2004.

XX PF 06-NOV-2003; 2003WO-US035268.

XX PR 08-NOV-2002; 2002US-0425235P.

XX PA (GETH) GENENTECH INC.

XX PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;

XX WPI; 2004-420067/39.

XX DR P-PSDB; AD019396.

XX PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthropathy.

XX PS Claim 1; SEQ ID NO 338; 1731pp; English.

XX CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polynucleotide of
 CC the invention.

XX SQ Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 6030;
 Best Local Similarity 80.0%; Pred. No. 14;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGCCUU 20
 |||||:||||:||||:
 Db 605 AACGGAGGCTGGGATGCCTT 624

RESULT 48
 ADR24647
 ID ADR24647 standard; DNA; 6030 BP.
 AC ADR24647;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Breast cancer prognosis marker #508.
 XX
 KW ds; breast cancer; prognosis; gene expression; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2004065545-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 15-JAN-2004; 2004WO-US001100.
 XX
 PR 15-JAN-2003; 2003US-00342887.
 XX
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 PA (NECA-) NETHERLANDS CANCER INST.
 XX
 PI Van't Veer LJ, He Y;
 XX
 DR WPI; 2004-593473/57.
 XX

PT Classifying a breast cancer patient according to prognosis comprises
 PT determining the similarity between the level of expression of each of
 PT five genes in a cell sample taken from patient, to control levels.
 XX
 PS Disclosure; SEQ ID NO 508; 226pp; English.
 XX
 CC The invention relates to a method of classifying a breast cancer patient
 CC according to prognosis by determining the similarity between the level of
 CC expression of each of five genes for which markers are listed in the
 CC specification, in a cell sample taken from the breast cancer patient, to
 CC control levels of expression for each respective five genes to obtain a
 CC patient similarity value. The methods are useful for classifying a breast
 CC cancer patient according to prognosis. Kits and computer program products
 CC are useful for data analysis using the diagnostic, prognostic and
 CC statistical methods of the invention. This sequence corresponds to a
 CC marker used in the method of the invention.
 XX

SEQ Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 13; Length 6030;
 Best Local Similarity 80.0%; Pred. No. 14;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGCCUU 20
 |||||:||||:||||:
 Db 605 AACGGAGGCTGGGATGCCTT 624

RESULT 49
 AAC84600
 ID AAC84600 standard; DNA; 6032 BP.
 XX
 AC AAC84600;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human BCL-2 protein encoding DNA.
 XX
 KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;

KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
 KW Bad; Bcl-2; tumour; cytostatic; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200075184-A1.
 XX
 PD 14-DEC-2000.
 XX
 PF 05-JUN-2000; 2000WO-US015449.
 XX
 PR 04-JUN-1999; 99US-0137494P.
 XX
 PA (UYVA) UNIV YALE.
 XX
 XX Zhang H, Tsvetkov LM, Kondo T;
 XX
 DR WPI; 2001-061703/07.
 DR P-PSDB; AAB48288.
 XX
 PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
 PT involves altering levels of proteins such as S-phase kinase associated
 PT proteins 1, 2 and cullin/CDC53 proteins.
 XX
 PS Example; Page 104-108; 162pp; English.
 XX

CC The invention relates to methods of altering the polypeptide levels in a
 CC cell, using proteins selected from S-phase kinase associated proteins 1
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
 CC cullin/ CDC53 family of proteins). The method is useful for altering the
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
 CC that modulate interactions between SKP and target proteins are useful for
 CC treating tumours
 CC

SEQ Sequence 6032 BP; 1670 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 6032;
 Best Local Similarity 80.0%; Pred. No. 14;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGCCUU 20
 |||||:||||:||||:
 Db 607 AACGGAGGCTGGGATGCCTT 626

RESULT 50
 ACN92553
 ID ACN92553 standard; DNA; 6142 BP.
 XX
 AC ACN92553;
 XX

DT 02-DEC-2004 (first entry)
 XX
 DE Breast cancer related marker, seq id 13703.
 XX

KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
 XX
 OS Homo sapiens.
 XX

PN US2003099974-A1.
 XX
 PD 29-MAY-2003.
 XX

PF 18-JUL-2002; 2002US-00198846.
 XX
 PR 18-JUL-2001; 2001US-0306220P.
 XX

PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Lillie J, Xu Y, Wang Y, Steinmann K;
 XX

DR WPI; 2003-787014/74.
 XX Novel isolated polypeptide associated with breast cancer, useful for
 PT detecting presence of polypeptide in sample, as a marker for breast
 PT cancer.
 XX
 PS Disclosure; SEQ ID NO 13703; 36pp; English.
 XX
 CC The invention relates to an isolated polypeptide (I) associated with
 CC breast cancer which is encoded by a nucleic acid molecule comprising a
 CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
 CC the polypeptide of the invention. The activity of the polypeptide of the
 CC invention may be described as cytostatic. The antibody is useful for
 CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
 CC invention are useful in the detection of breast tumours. (I) is useful as
 CC a marker for breast cancer and in breast cancer therapy. Sequences given
 CC in records ACN78851-ACN92934 represent nucleic acid markers associated
 CC with breast cancer. Note: The sequence listing does not form part of the
 CC specification but may be obtained in electronic format from the USPTO web
 CC site at seqdata.uspto.gov/sequence.html?DocID=20030099974
 XX
 SQ Sequence 6142 BP; 1696 A; 1273 C; 1418 G; 1747 T; 0 U; 8 Other;
 Query Match 100.0%; Score 20; DB 11; Length 6142;
 Best Local Similarity 80.0%; Pred.No. 14;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACGGAGGCTGGGATGCTT 709
 Db 690 AACGGAGGCTGGGATGCTT 709

Search completed: May 24, 2005, 04:57:17
 Job time : 514 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 04:26:18 ; Search time 3114 Seconds
(without alignments)
244.472 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacggaggcugggaugccuu 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 750 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gest1.*
9: gb_gest2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	423	5	BY283543
2	20	100.0	424	4	BM193252
3	20	100.0	453	4	BM193253
4	20	100.0	471	7	CO615208
5	20	100.0	493	2	BB858352
6	20	100.0	497	7	CO622375
7	20	100.0	500	9	AY416380
8	20	100.0	503	7	CO624236
9	20	100.0	536	7	CO618349
10	20	100.0	545	7	CO633169
11	20	100.0	602	1	AL703462
12	20	100.0	613	2	BF195698
13	20	100.0	627	7	CO708923
14	20	100.0	685	2	BB409769
15	20	100.0	711	9	AY416381
16	20	100.0	720	9	AY416379
17	20	100.0	747	2	BF448405
18	20	100.0	786	1	AU135900
19	20	100.0	908	6	CB556236
20	20	100.0	2354	3	AK049473
21	19	95.0	574	2	AW418903
22	18.4	92.0	487	6	CA964607
23	18.4	92.0	492	2	BB695602
24	18.4	92.0	513	4	BM363392

25	18.4	92.0	523	2	BB771745
26	17.4	92.0	593	1	AI981239
27	17.4	87.0	437	7	W16827
28	17.4	87.0	627	7	CV067685
29	17.4	87.0	665	7	CV222414
30	17.4	87.0	892	7	CK985413
31	17	85.0	366	5	BY412675
32	17	85.0	398	8	AQ095759
33	17	85.0	784	9	AG583207
34	16.8	84.0	252	7	CF113630
35	16.8	84.0	311	9	CG579617
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37	16.8	84.0	382	2	BF544522
38	16.8	84.0	382	4	BF554221
39	16.8	84.0	396	4	BF518513
40	16.8	84.0	452	1	AA352879
41	16.8	84.0	468	7	R94119
42	16.8	84.0	471	5	BU641963
43	16.8	84.0	497	1	AA352677
44	16.8	84.0	509	5	BY394530
45	16.8	84.0	539	4	BM867198
46	16.8	84.0	545	6	CD031828
47	16.8	84.0	600	4	BM866514
48	16.8	84.0	655	5	BQ391811
49	16.8	84.0	670	9	AG110319
50	16.8	84.0	677	9	CE276116
51	16.8	84.0	704	7	CK359399
52	16.8	84.0	732	7	CO569038
53	16.8	84.0	752	7	CK358038
54	16.8	84.0	756	9	CC532659
55	16.8	84.0	762	7	CK367683
56	16.8	84.0	763	6	CB987262
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58	16.8	84.0	789	7	CF153265
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60	16.8	84.0	813	6	CD619038
61	16.8	84.0	821	6	CB231334
62	16.8	84.0	840	7	CF152830
63	16.8	84.0	840	7	CF152830
64	16.8	84.0	854	7	CF377358
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66	16.8	84.0	1042	5	BQ071421
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68	16.8	84.0	1241	9	AG121473
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70	16.4	82.0	452	6	BY572443
71	16.4	82.0	567	9	CE502639
72	16.4	82.0	589	7	CO684249
73	16.4	82.0	646	2	BE303767
74	16.4	82.0	699	9	AG340150
75	16.4	82.0	705	9	AG009689
76	16.4	82.0	758	9	AG456439
77	16.4	82.0	771	9	AG554199
78	16.4	82.0	1439	4	EG764408
79	16.4	82.0	3495	3	AK030347
80	16.4	82.0	3566	3	AK090330
81	16.4	82.0	3881	3	AK050075
82	16.4	82.0	6327	3	AK019470
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87	16	80.0	586	2	BF205472
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90	16	80.0	631	5	BQ476976
91	16	80.0	651	5	CA591070
92	16	80.0	682	5	BQ476870
93	16	80.0	735	2	BE268254
94	16	80.0	750	4	BI185743
95	16	80.0	759	9	CC915206
96	16	80.0	836	2	BE560128
97	16	80.0	896	7	CO774263

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AI981239	pat.pk004
W16827	zb11f01.r1
CV067685	Le_mx0_37
CV222414	Le_mx0_60
CK985413	VTET8_Ch
BY412675	BY412675
AQ095759	HS_3013_B
AG583207	Mus muscu
CF113630	Shultzomi
CG579617	OST218114
CD028860	mgmy005x0
BF544522	UI-R-BT0-
BF554221	UI-R-CO-h
BF518513	603061632
AA352879	EST61011
R94119	vt74606.r1
BU641963	mgmk010xE
AA352677	EST60704
BY394530	BY394530
BM867198	mgc8009x0
CD031828	mgmt007xD
BM866514	mgc8006xC
BQ391811	NISC_mg20
AG110319	Pan trogl
CE276116	tigr-g88-
CK359399	AGNCOURT
CO569038	AGNCOURT
CK358038	AGNCOURT
CC532659	CH240_410
CK367683	AGNCOURT
CB987262	AGNCOURT
CV080644	AGNCOURT
CF153265	AGNCOURT
BX734553	BX734553
CD619038	AUP_104_G
CB231334	AGNCOURT
CF153185	AGNCOURT
CF152830	AGNCOURT
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CL296243	ZMMBB002
BQ071421	AGNCOURT
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AG121473	Pan trogl
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AG340150	Mus muscu
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AK030347	Mus muscu
AK090330	Mus muscu
AK050075	Mus muscu
AK019470	Mus muscu
BQ621457	TVEST005
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BP525013	BP525013
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BM041926	RPCI-24-2
BQ476976	metadama6
CA591070	hels34f05
BQ476870	metadama3
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CC915206	t086j06ba
BE560128	601346803
CO774263	ILLUMIGEN

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c 100	16	80.0	1014	7	CF217162	AGENCOURT	CF217162	c 173	15.8	79.0	563	8	AQ49376	AQ49376	AQ49376	AQ49376
c 101	16	80.0	5141	3	AK029539	MUS muscu	AK029539	c 174	15.8	79.0	566	8	AO397936	AO397936	AO397936	AO397936
c 102	15.8	79.0	179	1	AU238697	AU238697	AU238697	c 175	15.8	79.0	567	9	CO520437	CO520437	CO520437	CO520437
c 103	15.8	79.0	243	2	BF543538	UI-R-C3-t	BF543538	c 176	15.8	79.0	567	9	CE401647	CE401647	CE401647	CE401647
c 104	15.8	79.0	282	7	CN869890	001203AAO	CN869890	c 177	15.8	79.0	574	3	CR709942	CR709942	CR709942	CR709942
c 105	15.8	79.0	286	1	AA378562	EST91299	AA378562	c 178	15.8	79.0	574	3	CL744963	CL744963	CL744963	CL744963
c 106	15.8	79.0	336	5	BY373192	BY373192	BY373192	c 179	15.8	79.0	581	5	BU637370	BU637370	BU637370	BU637370
c 107	15.8	79.0	340	1	CL559260	OB_Ba001	CL559260	c 180	15.8	79.0	581	5	BU637370	BU637370	BU637370	BU637370
c 108	15.8	79.0	348	1	AI756934	EEESTea03	AI756934	c 181	15.8	79.0	586	9	CL780633	CL780633	CL780633	CL780633
c 109	15.8	79.0	355	5	BY223361	BY223361	BY223361	c 182	15.8	79.0	588	1	AA520762	AA520762	AA520762	AA520762
c 110	15.8	79.0	356	1	AA335406	EST62268	AA335406	c 183	15.8	79.0	590	5	BQ390503	BQ390503	BQ390503	BQ390503
c 111	15.8	79.0	357	6	CD713128	4041042_1	CD713128	c 184	15.8	79.0	596	4	BM488510	BM488510	BM488510	BM488510
c 112	15.8	79.0	374	1	AI1120090	uc27607_z	AI1120090	c 185	15.8	79.0	602	1	AL970361	AL970361	AL970361	AL970361
c 113	15.8	79.0	382	8	B411708	HS-1054-A2-	B411708	c 186	15.8	79.0	602	8	AQ435070	AQ435070	AQ435070	AQ435070
c 114	15.8	79.0	384	1	AI6755575	AJ6755575	AI6755575	c 187	15.8	79.0	603	1	AJ737419	AJ737419	AJ737419	AJ737419
c 115	15.8	79.0	385	4	BI016476	PM1-BT026	BI016476	c 188	15.8	79.0	606	9	CL784010	CL784010	CL784010	CL784010
c 116	15.8	79.0	390	6	CA546923	K0139B01-	CA546923	c 189	15.8	79.0	608	9	CE078619	CE078619	CE078619	CE078619
c 117	15.8	79.0	393	5	BP614098	BP614098	BP614098	c 190	15.8	79.0	614	9	CG840588	CG840588	CG840588	CG840588
c 118	15.8	79.0	398	5	BY395173	BY395173	BY395173	c 191	15.8	79.0	616	9	DR24K78	DR24K78	DR24K78	DR24K78
c 119	15.8	79.0	400	6	CA545812	K012B01-	CA545812	c 192	15.8	79.0	617	4	BI249172	BI249172	BI249172	BI249172
c 120	15.8	79.0	404	1	AA307238	EST178139	AA307238	c 193	15.8	79.0	624	4	BM867804	BM867804	BM867804	BM867804
c 121	15.8	79.0	406	7	CN573781	rc42h07_x	CN573781	c 194	15.8	79.0	627	6	CB447652	CB447652	CB447652	CB447652
c 122	15.8	79.0	408	1	AA076339	zm18g10_r	AA076339	c 195	15.8	79.0	629	5	BU447903	BU447903	BU447903	BU447903
c 123	15.8	79.0	442	5	BY359631	BY359631	BY359631	c 196	15.8	79.0	630	6	CA294515	CA294515	CA294515	CA294515
c 124	15.8	79.0	447	5	BP613171	BP613171	BP613171	c 197	15.8	79.0	632	1	AL959700	AL959700	AL959700	AL959700
c 125	15.8	79.0	450	4	EG373211	UI-R-CV1-	EG373211	c 198	15.8	79.0	632	1	BE271923	BE271923	BE271923	BE271923
c 126	15.8	79.0	463	5	BP611505	BP611505	BP611505	c 199	15.8	79.0	652	6	CB689514	CB689514	CB689514	CB689514
c 127	15.8	79.0	464	8	AQ650177	Sheared D	AQ650177	c 200	15.8	79.0	656	1	AA950307	AA950307	AA950307	AA950307
c 128	15.8	79.0	468	1	AA671751	v105g05_r	AA671751	c 201	15.8	79.0	666	5	BU477240	BU477240	BU477240	BU477240
c 129	15.8	79.0	468	6	BY546231	BY546231	BY546231	c 202	15.8	79.0	674	7	CO422130	CO422130	CO422130	CO422130
c 130	15.8	79.0	471	6	CA545364	K0112B03-	CA545364	c 203	15.8	79.0	674	8	BR934889	BR934889	BR934889	BR934889
c 131	15.8	79.0	471	6	CA686714	wlm96.pk0	CA686714	c 204	15.8	79.0	676	4	BI391438	BI391438	BI391438	BI391438
c 132	15.8	79.0	478	8	AQ839727	HS_4730_A	AQ839727	c 205	15.8	79.0	680	5	BU637281	BU637281	BU637281	BU637281
c 133	15.8	79.0	479	9	CL629254	OR_BBa002	CL629254	c 206	15.8	79.0	690	7	CF883418	CF883418	CF883418	CF883418
c 134	15.8	79.0	481	9	CG519915	CG519915	CG519915	c 207	15.8	79.0	690	8	AQ399902	AQ399902	AQ399902	AQ399902
c 135	15.8	79.0	487	1	BZ656230	OGAML85NC	BZ656230	c 208	15.8	79.0	703	1	AI982008	AI982008	AI982008	AI982008
c 136	15.8	79.0	487	8	AA241279	nv31c06_r	AA241279	c 209	15.8	79.0	705	8	BE680918	BE680918	BE680918	BE680918
c 137	15.8	79.0	491	6	CD727479	4032302_r	CD727479	c 210	15.8	79.0	715	6	BY751214	BY751214	BY751214	BY751214
c 138	15.8	79.0	491	9	CG176959	FUIDD647D	CG176959	c 211	15.8	79.0	717	1	AJ455133	AJ455133	AJ455133	AJ455133
c 139	15.8	79.0	495	4	BG514115	dacl17h03_r	BG514115	c 212	15.8	79.0	717	1	CO891526	CO891526	CO891526	CO891526
c 140	15.8	79.0	503	6	CA824721	R47B09_t	CA824721	c 213	15.8	79.0	722	2	BE397189	BE397189	BE397189	BE397189
c 141	15.8	79.0	503	7	CR538980	DKF2p459L	CR538980	c 214	15.8	79.0	722	8	CG319293	CG319293	CG319293	CG319293
c 142	15.8	79.0	504	7	CR868765	001117AAO	CR868765	c 215	15.8	79.0	723	9	CL727631	CL727631	CL727631	CL727631
c 143	15.8	79.0	505	3	CNS0A0AF	Arabidops	EX833508	c 216	15.8	79.0	727	5	BU421605	BU421605	BU421605	BU421605
c 144	15.8	79.0	505	3	CNS09Z1W	Arabidops	EX832940	c 217	15.8	79.0	730	5	BU453655	BU453655	BU453655	BU453655
c 145	15.8	79.0	512	8	AQ188064	HS_3164_A	AQ188064	c 218	15.8	79.0	732	8	AQ688736	AQ688736	AQ688736	AQ688736
c 146	15.8	79.0	513	5	BM900292	rc17a02_y	BM900292	c 219	15.8	79.0	738	9	BX173814	BX173814	BX173814	BX173814
c 147	15.8	79.0	515	5	BM883978	rc18a03_y	BM883978	c 220	15.8	79.0	741	1	AJ446603	AJ446603	AJ446603	AJ446603
c 148	15.8	79.0	516	4	BM868482	ngc8014xd	BM868482	c 221	15.8	79.0	745	6	CB909557	CB909557	CB909557	CB909557
c 149	15.8	79.0	520	1	AI549161	UI-R-C3-t	AI549161	c 222	15.8	79.0	746	4	BI654291	BI654291	BI654291	BI654291
c 150	15.8	79.0	520	3	CNS09YNS	Arabidops	EX833361	c 223	15.8	79.0	756	9	CC701789	CC701789	CC701789	CC701789
c 151	15.8	79.0	520	4	BJ066350	BJ066350	BJ066350	c 224	15.8	79.0	756	5	BX749328	BX749328	BX749328	BX749328
c 152	15.8	79.0	524	8	AQ287088	mgx0017j	AQ287088	c 225	15.8	79.0	757	8	BH356549	BH356549	BH356549	BH356549
c 153	15.8	79.0	526	5	BM900911	rc42h07_y	BM900911	c 226	15.8	79.0	758	5	BU246514	BU246514	BU246514	BU246514
c 154	15.8	79.0	526	7	CK931451	p5mgc_00	CK931451	c 227	15.8	79.0	764	5	BU476977	BU476977	BU476977	BU476977
c 155	15.8	79.0	528	1	AA048699	mj33h08_r	AA048699	c 228	15.8	79.0	782	7	CV114613	CV114613	CV114613	CV114613
c 156	15.8	79.0	528	6	CA544522	K0100F07-	CA544522	c 229	15.8	79.0	786	9	AG426356	AG426356	AG426356	AG426356
c 157	15.8	79.0	529	6	CD733828	4046743_1	CD733828	c 230	15.8	79.0	794	9	CL133590	CL133590	CL133590	CL133590
c 158	15.8	79.0	529	9	CL333801	RPC144_25	CL333801	c 231	15.8	79.0	795	1	AJ731843	AJ731843	AJ731843	AJ731843
c 159	15.8	79.0	531	9	CL744780	OR_BBa008	CL744780	c 232	15.8	79.0	795	7	CN230173	CN230173	CN230173	CN230173
c 160	15.8	79.0	534	4	BG514103	daC17f11_r	BG514103	c 233	15.8	79.0	799	5	BU381568	BU381568	BU381568	BU381568
c 161	15.8	79.0	537	8	BH755585	SALK_0518	BH755585	c 234	15.8	79.0	801	7	CF151477	CF151477	CF151477	CF151477
c 162	15.8	79.0	539	5	BM884572	rc13f08_y	BM884572	c 235	15.8	79.0	802	5	BU259516	BU259516	BU259516	BU259516
c 163	15.8	79.0	542	7	CN902392	021014ABC	CN902392	c 236	15.8	79.0	802	5	BU321008	BU321008	BU321008	BU321008
c 164	15.8	79.0	543	2	BF193671	245338_MA	BF193671	c 237	15.8	79.0	805	7	BU253434	BU253434	BU253434	BU253434
c 165	15.8	79.0	550	8	BZ656234	OGAML85TM	BZ656234	c 238	15.8	79.0	808	5	CN236190	CN236190	CN236190	CN236190
c 166	15.8	79.0	553	7	CF893029	A0117H12-	CF893029	c 239	15.8	79.0	817	9	CG223679	CG223679	CG223679	CG223679
c 167	15.8	79.0	554	3	CR711090	Tetraodon	CR711090	c 240	15.8	79.0	832	5	BU137043	BU137043	BU137043	BU137043
c 168	15.8	79.0	554	8	AZ621580	IM0454D24	AZ621580	c 241	15.8	79.0	837	8	BZ771294	BZ771294	BZ771294	BZ771294
c 169	15.8	79.0	555	3	CR718271	Tetraodon	CR718271	c 242	15.8	79.0	840	1	AJ568670	AJ568670	AJ568670	AJ568670
c 170	15.8	79.0	559	9	CL32808											

c 244	15.8	79.0	867	6	CD254471	AGENCY	317	15.4	77.0	420	6	BY675756	BY675756
c 245	15.8	79.0	870	7	CO932513	AGENCY	c 318	15.4	77.0	424	5	BP745570	BP745570
c 246	15.8	79.0	871	5	BU956649	AGENCY	c 319	15.4	77.0	433	5	BQ025679	BQ025679
c 247	15.8	79.0	873	7	CC905015	CO180909	c 320	15.4	77.0	435	4	BM778315	BM778315
c 248	15.8	79.0	878	7	CO489504	CO202557	c 321	15.4	77.0	438	4	BM712790	BM712790
c 249	15.8	79.0	901	9	CL067637	CH216-111	c 322	15.4	77.0	441	1	AI852013	AI852013
c 250	15.8	79.0	906	5	BU318500	BU318500	c 323	15.4	77.0	444	7	RI7732	RI7732
c 251	15.8	79.0	917	5	CNS03NP1	CO180909	c 324	15.4	77.0	453	1	AI684816	AI684816
c 252	15.8	79.0	918	2	BF163432	BF163432	c 325	15.4	77.0	465	9	CG663467	CG663467
c 253	15.8	79.0	928	4	BI524958	BI524958	c 326	15.4	77.0	465	9	AJ727260	AJ727260
c 254	15.8	79.0	928	9	CL119317	CL119317	c 327	15.4	77.0	470	5	BX110392	BX110392
c 255	15.8	79.0	933	5	BU152179	BU152179	c 328	15.4	77.0	472	5	BP754496	BP754496
c 256	15.8	79.0	938	7	CF411903	CF411903	c 329	15.4	77.0	474	6	BY561267	BY561267
c 257	15.8	79.0	939	9	CG863539	CG863539	c 330	15.4	77.0	481	1	AI237509	AI237509
c 258	15.8	79.0	942	5	BU461722	BU461722	c 331	15.4	77.0	481	5	BP532094	BP532094
c 259	15.8	79.0	951	9	CL109139	CL109139	c 332	15.4	77.0	489	4	BI997595	BI997595
c 260	15.8	79.0	956	9	CG770849	CG770849	c 333	15.4	77.0	491	7	CK685606	CK685606
c 261	15.8	79.0	960	4	BG764642	BG764642	c 334	15.4	77.0	491	8	AZ242110	AZ242110
c 262	15.8	79.0	967	9	CL077961	CL077961	c 335	15.4	77.0	497	1	AA530726	AA530726
c 263	15.8	79.0	971	4	BG292543	BG292543	c 336	15.4	77.0	499	7	CK451009	CK451009
c 264	15.8	79.0	982	7	CK424841	CK424841	c 337	15.4	77.0	499	7	CK454259	CK454259
c 265	15.8	79.0	987	5	BU463919	BU463919	c 338	15.4	77.0	499	7	CK457467	CK457467
c 266	15.8	79.0	1009	9	CL086939	CL086939	c 339	15.4	77.0	499	7	CK459209	CK459209
c 267	15.8	79.0	1048	9	CL118371	CL118371	c 340	15.4	77.0	500	1	AA189618	AA189618
c 268	15.8	79.0	1055	5	EX405345	EX405345	c 341	15.4	77.0	501	2	BE655351	BE655351
c 269	15.8	79.0	1081	9	CNS05E7D	CNS05E7D	c 342	15.4	77.0	503	5	BQ105279	BQ105279
c 270	15.8	79.0	1095	5	BU335411	BU335411	c 343	15.4	77.0	503	7	CO578250	CO578250
c 271	15.8	79.0	1124	8	CC285183	CC285183	c 344	15.4	77.0	511	7	CK069477	CK069477
c 272	15.8	79.0	1171	7	CO635511	CO635511	c 345	15.4	77.0	511	9	CK492170	CK492170
c 273	15.8	79.0	1179	7	CC227506	CC227506	c 346	15.4	77.0	512	2	BB795953	BB795953
c 274	15.8	79.0	1187	5	BU520251	BU520251	c 347	15.4	77.0	513	8	AZ990132	AZ990132
c 275	15.8	79.0	1205	3	AK037053	AK037053	c 348	15.4	77.0	519	8	AQ762647	AQ762647
c 276	15.8	79.0	1768	3	AK043959	AK043959	c 349	15.4	77.0	522	2	AW180522	AW180522
c 277	15.4	77.0	193	2	AW416438	AW416438	c 350	15.4	77.0	524	4	BI720580	BI720580
c 278	15.4	77.0	260	1	AL716898	AL716898	c 351	15.4	77.0	527	8	AZ097509	AZ097509
c 279	15.4	77.0	262	1	AA378896	AA378896	c 352	15.4	77.0	527	9	CK160870	CK160870
c 280	15.4	77.0	285	7	Z46976	Z46976	c 353	15.4	77.0	541	9	CR234203	CR234203
c 281	15.4	77.0	303	7	R18576	R18576	c 354	15.4	77.0	542	9	EX981241	EX981241
c 282	15.4	77.0	303	9	CG473320	CG473320	c 355	15.4	77.0	543	1	AJ741437	AJ741437
c 283	15.4	77.0	304	7	F13538	F13538	c 356	15.4	77.0	543	8	AZ018717	AZ018717
c 284	15.4	77.0	305	6	CB838714	CB838714	c 357	15.4	77.0	551	9	CG586256	CG586256
c 285	15.4	77.0	311	2	AW428388	AW428388	c 358	15.4	77.0	553	7	CF753210	CF753210
c 286	15.4	77.0	311	1	AA198514	AA198514	c 359	15.4	77.0	554	4	BQ093737	BQ093737
c 287	15.4	77.0	321	9	CL965561	CL965561	c 360	15.4	77.0	555	7	CK069476	CK069476
c 288	15.4	77.0	353	7	R14769	R14769	c 361	15.4	77.0	557	1	AL701271	AL701271
c 289	15.4	77.0	355	4	BF956163	BF956163	c 362	15.4	77.0	557	8	AQ815248	AQ815248
c 290	15.4	77.0	355	4	BF956163	BF956163	c 363	15.4	77.0	558	2	BF042817	BF042817
c 291	15.4	77.0	360	2	AW347290	AW347290	c 364	15.4	77.0	559	8	AZ700607	AZ700607
c 292	15.4	77.0	367	2	BF362064	BF362064	c 365	15.4	77.0	563	9	EX970363	EX970363
c 293	15.4	77.0	367	5	BY373434	BY373434	c 366	15.4	77.0	568	9	CG592547	CG592547
c 294	15.4	77.0	369	8	B88104	B88104	c 367	15.4	77.0	570	2	BF023367	BF023367
c 295	15.4	77.0	375	4	BF956308	BF956308	c 368	15.4	77.0	571	4	BI995640	BI995640
c 296	15.4	77.0	375	7	CO780890	CO780890	c 369	15.4	77.0	578	2	AW180587	AW180587
c 297	15.4	77.0	376	2	BB813502	BB813502	c 370	15.4	77.0	579	9	CE839763	CE839763
c 298	15.4	77.0	377	2	AW428397	AW428397	c 371	15.4	77.0	580	7	CK184000	CK184000
c 299	15.4	77.0	381	6	BY528365	BY528365	c 372	15.4	77.0	583	6	CD612009	CD612009
c 300	15.4	77.0	382	1	AA718576	AA718576	c 373	15.4	77.0	584	1	AV667268	AV667268
c 301	15.4	77.0	385	2	BF376342	BF376342	c 374	15.4	77.0	586	1	AL970060	AL970060
c 302	15.4	77.0	389	1	AI852018	AI852018	c 375	15.4	77.0	587	5	BP772038	BP772038
c 303	15.4	77.0	390	5	BY698748	BY698748	c 376	15.4	77.0	589	4	BI181301	BI181301
c 304	15.4	77.0	397	6	BU610923	BU610923	c 377	15.4	77.0	589	5	BK277022	BK277022
c 305	15.4	77.0	398	4	BG021538	BG021538	c 378	15.4	77.0	591	4	BI874056	BI874056
c 306	15.4	77.0	399	2	B8816642	B8816642	c 379	15.4	77.0	598	2	BE967412	BE967412
c 307	15.4	77.0	399	5	BY105179	BY105179	c 380	15.4	77.0	598	8	BZ256489	BZ256489
c 308	15.4	77.0	400	5	EX639575	EX639575	c 381	15.4	77.0	603	5	BQ814450	BQ814450
c 309	15.4	77.0	401	2	BB804269	BB804269	c 382	15.4	77.0	607	5	BU647500	BU647500
c 310	15.4	77.0	401	4	BG975519	BG975519	c 383	15.4	77.0	608	5	BP753898	BP753898
c 311	15.4	77.0	403	2	BF318176	BF318176	c 384	15.4	77.0	610	9	CR091096	CR091096
c 312	15.4	77.0	403	2	BF452174	BF452174	c 385	15.4	77.0	611	5	BU322869	BU322869
c 313	15.4	77.0	412	1	AA916788	AA916788	c 386	15.4	77.0	612	7	CF791591	CF791591
c 314	15.4	77.0	414	2	AW480364	AW480364	c 387	15.4	77.0	613	5	BU647499	BU647499
c 315	15.4	77.0	416	2	BB824262	BB824262	c 388	15.4	77.0	617	9	CR201150	CR201150
c 316	15.4	77.0	420	2	BB788684	BB788684	c 389	15.4	77.0	619	6	CB836308	CB836308

c 390	15.4	77.0	620	5	BU459297	603366231	c 463	15.4	77.0	787	5	BU446419	603214205
c 391	15.4	77.0	626	1	AL878719	AL878719	c 464	15.4	77.0	796	9	CR101933	Forward s
c 392	15.4	77.0	628	1	AJ637305	AJ637305	c 465	15.4	77.0	799	2	BF531726	BF531726
c 393	15.4	77.0	628	5	BX275424	BX275424	c 466	15.4	77.0	799	7	CF826301	EST703683
c 394	15.4	77.0	629	7	CV030213	9254 Full	c 467	15.4	77.0	804	4	BM051178	603634115
c 395	15.4	77.0	629	7	CV094116	FAMU USDA	c 468	15.4	77.0	805	5	BX277023	BX277023
c 396	15.4	77.0	630	7	CN745340	SAL_US009	c 469	15.4	77.0	817	9	BX983063	Reverse s
c 397	15.4	77.0	631	8	BZ939650	CH240_106	c 470	15.4	77.0	836	4	BI831230	603080693
c 398	15.4	77.0	632	6	CD029982	mgmt001XA	c 471	15.4	77.0	837	4	BI147839	602912725
c 399	15.4	77.0	635	1	AL888406	AL888406	c 472	15.4	77.0	838	7	CK846499	969004 MA
c 400	15.4	77.0	641	1	AJ399424	AJ399424	c 473	15.4	77.0	843	9	AG162148	Pan trogl
c 401	15.4	77.0	641	8	AZ593803	IM0405102	c 474	15.4	77.0	849	6	CD792311	EST663672
c 402	15.4	77.0	643	1	AJ448555	AJ448555	c 475	15.4	77.0	852	7	CN231295	WLB061005
c 403	15.4	77.0	648	1	AL873788	AL873788	c 476	15.4	77.0	860	6	CA184136	CA184136
c 404	15.4	77.0	651	5	BQ0808109	1030001H0	c 477	15.4	77.0	875	9	CG114416	PURFX94TD
c 405	15.4	77.0	659	4	BI831251	603080518	c 478	15.4	77.0	878	6	CB997612	AGENCOURT
c 406	15.4	77.0	663	9	AG134255	Pan trogl	c 479	15.4	77.0	887	2	B8665984	601678413
c 407	15.4	77.0	664	8	BZ433839	BZ433839	c 480	15.4	77.0	888	1	AJ721758	AJ721758
c 408	15.4	77.0	665	1	AJ721752	SONNT25TR	c 481	15.4	77.0	895	7	CF812290	EST689672
c 409	15.4	77.0	666	7	CO429481	UI-M-HW0-	c 482	15.4	77.0	895	7	CF826649	EST704031
c 410	15.4	77.0	667	1	AL631928	AL631928	c 483	15.4	77.0	896	9	CG114415	PURFX94TB
c 411	15.4	77.0	669	2	BB149254	BB149254	c 484	15.4	77.0	897	5	BQ957869	AGENCOURT
c 412	15.4	77.0	673	5	BP434376	BP434376	c 485	15.4	77.0	899	9	CNS06Z05	AL421707 T7 end of
c 413	15.4	77.0	675	1	AL869322	AL869322	c 486	15.4	77.0	906	9	CL960740	OS1PCC037
c 414	15.4	77.0	679	9	AG009562	Homo sapi	c 487	15.4	77.0	909	5	BX328977	BX328977
c 415	15.4	77.0	679	5	BP510660	BP510660	c 488	15.4	77.0	909	6	CD557807	AGENCOURT
c 416	15.4	77.0	680	1	AL595866	AL595866	c 489	15.4	77.0	910	5	BX327692	BX327692
c 417	15.4	77.0	680	1	AV091287	AV091287	c 490	15.4	77.0	927	4	BM816858	HB105D02
c 418	15.4	77.0	681	2	AW651123	833001F10	c 491	15.4	77.0	927	7	CK287837	EST750559
c 419	15.4	77.0	681	7	CO577675	TVEST081H	c 492	15.4	77.0	937	6	CD243304	AGENCOURT
c 420	15.4	77.0	685	4	BI868833	603391994	c 493	15.4	77.0	946	5	BX342958	BX342958
c 421	15.4	77.0	685	6	CB171743	BZ1603020	c 494	15.4	77.0	955	2	BF142698	601789944
c 422	15.4	77.0	690	7	CF732739	UI-M-HW0-	c 495	15.4	77.0	973	9	CNS04DVZ	AL286280 Tetraodon
c 423	15.4	77.0	691	7	CK173897	EST763217	c 496	15.4	77.0	982	4	BM449761	AGENCOURT
c 424	15.4	77.0	692	7	CO429503	CO429503	c 497	15.4	77.0	990	5	BX328976	BX328976
c 425	15.4	77.0	696	4	BG854708	1024040F0	c 498	15.4	77.0	1001	4	BG036474	602326421
c 426	15.4	77.0	696	6	CB524981	UI-M-FY0-	c 499	15.4	77.0	1013	8	CC298405	CH261-73J
c 427	15.4	77.0	697	9	AG009661	AG009661	c 500	15.4	77.0	1023	4	BI555251	603236002
c 428	15.4	77.0	703	5	BQ443673	BQ443673	c 501	15.4	77.0	1039	6	CD792310	EST663671
c 429	15.4	77.0	704	6	CB836247	CB836247	c 502	15.4	77.0	1059	9	CNS048S9	AL279666 Tetraodon
c 430	15.4	77.0	709	6	CB835686	CB835686	c 503	15.4	77.0	1097	8	CC304525	CH261-134
c 431	15.4	77.0	710	1	AJ831869	AJ831869	c 504	15.4	77.0	1101	9	CNS0035W	AL064399 Drosophila
c 432	15.4	77.0	710	7	CF445363	CF445363	c 505	15.4	77.0	1121	4	BM553010	BM553010
c 433	15.4	77.0	710	7	CO428727	CO428727	c 506	15.4	77.0	1171	4	BG335642	602404268
c 434	15.4	77.0	711	9	BX988240	Reverse s	c 507	15.4	77.0	1191	9	AY410693	AY410693
c 435	15.4	77.0	715	1	AJ832037	AJ832037	c 508	15.4	77.0	1460	5	BM926129	AGENCOURT
c 436	15.4	77.0	718	6	CD298013	CD298013	c 509	15.4	77.0	1461	4	BG481574	602528489
c 437	15.4	77.0	718	9	CC554610	CH240_461	c 510	15.4	77.0	1538	3	CR598985	full-leng
c 438	15.4	77.0	722	5	BM943993	BM943993	c 511	15.4	77.0	1675	3	AK012440	Mus muscu
c 439	15.4	77.0	725	4	BI831297	BI831297	c 512	15.4	77.0	1912	3	CR602224	CR602224
c 440	15.4	77.0	726	9	AG440721	Mus muscu	c 513	15.4	77.0	2668	3	AK090349	Mus muscu
c 441	15.4	77.0	727	4	BG854709	BG854709	c 514	15.4	77.0	2820	3	AK034118	AK034118
c 442	15.4	77.0	731	5	BM947251	UI-M-EH0p	c 515	15.4	77.0	2823	3	AK033956	Mus muscu
c 443	15.4	77.0	734	9	AG134925	AG134925	c 516	15.4	77.0	3162	3	AK043638	Mus muscu
c 444	15.4	77.0	736	5	BU110640	BU110640	c 517	15.4	77.0	3421	3	AK031092	AK031092
c 445	15.4	77.0	738	4	BI248130	602960882	c 518	15.4	77.0	3525	3	AK048607	AK048607
c 446	15.4	77.0	738	7	CN747215	SAL_US025	c 519	15.4	77.0	3831	3	AK036161	AK036161
c 447	15.4	77.0	738	9	AG405565	Mus muscu	c 520	15.4	77.0	4023	3	AK090391	AK090391
c 448	15.4	77.0	739	7	CO429401	CO429401	c 521	15.2	76.0	114	9	CL437358	PST5182-N
c 449	15.4	77.0	740	8	BZ203007	CH230-445	c 522	15.2	76.0	152	1	AA170094	AA170094
c 450	15.4	77.0	741	9	BJ731590	BJ731590	c 523	15.2	76.0	154	1	AA746989	AA746989
c 451	15.4	77.0	741	9	AG148544	AG148544	c 524	15.2	76.0	156	2	BF870039	BF870039
c 452	15.4	77.0	744	5	BM944475	UI-M-EH0p	c 525	15.2	76.0	156	4	BJ523749	BJ523749
c 453	15.4	77.0	747	7	CF733674	CF733674	c 526	15.2	76.0	172	1	AA370254	AA370254
c 454	15.4	77.0	753	4	BI199788	BI199788	c 527	15.2	76.0	182	6	CB423805	CB423805
c 455	15.4	77.0	756	6	CD240952	CD240952	c 528	15.2	76.0	192	6	CF074115	PE1_21_C0
c 456	15.4	77.0	757	6	CA315617	UI-M-FW0-	c 529	15.2	76.0	216	4	BM818607	BM818607
c 457	15.4	77.0	757	6	CA323442	UI-M-FX0-	c 530	15.2	76.0	231	2	BF806802	K-EST0085
c 458	15.4	77.0	766	7	CB244640	UI-M-FW0-	c 531	15.2	76.0	231	5	BP684959	BP684959
c 459	15.4	77.0	766	7	CO427998	UI-M-FW0-	c 532	15.2	76.0	232	2	BF804861	BF804861
c 460	15.4	77.0	770	4	BI821548	BI821548	c 533	15.2	76.0	239	2	BI182923	BI182923
c 461	15.4	77.0	770	5	BU408206	603485382	c 534	15.2	76.0	241	1	AV150477	AV150477
c 462	15.4	77.0	784	7	CK481984	AGENCOURT	c 535	15.2	76.0	256	7	CR556066	DKF2p4690

682	15.2	76.0	1	AI154309	AI154309 ud31c05.r
c 683	15.2	76.0	465	AI536822	TO80H08.x
684	15.2	76.0	466	AQ685080	HS 2160 A
c 685	15.2	76.0	466	CG646082	OST391457
686	15.2	76.0	470	BI472448	fs03e02.y
c 687	15.2	76.0	473	BB745700	BB745700
c 688	15.2	76.0	475	BY591219	BY591219
689	15.2	76.0	476	AQ210545	HS 2212 A
c 690	15.2	76.0	478	BX529982	BX529982
691	15.2	76.0	482	BE457643	us94e10.x
692	15.2	76.0	482	CO892748	Bovgen_21
c 693	15.2	76.0	483	CN365674	170005325
c 694	15.2	76.0	485	BE589479	195667 BA
c 695	15.2	76.0	486	AW814883	MR1-STP030
696	15.2	76.0	487	CK105304	1082P93.5
c 697	15.2	76.0	488	BM221690	K0108E03-
698	15.2	76.0	488	AZ929255	479.dif24
699	15.2	76.0	489	AG982977	PM0-CN015
700	15.2	76.0	489	CE784953	tigr-gss-
701	15.2	76.0	489	CE784953	tigr-gss-
702	15.2	76.0	491	CC984916	ZUAER67TV
c 703	15.2	76.0	492	AA527543	RG38c05.8
c 704	15.2	76.0	492	CB538940	777036 MA
705	15.2	76.0	493	CK336659	C0241F11-
c 706	15.2	76.0	494	CV432176	RT0230 Ch
707	15.2	76.0	495	BY365859	BY365859
c 708	15.2	76.0	497	CA601661	wr1.pk000
c 709	15.2	76.0	497	BM214324	Cm f5b001
710	15.2	76.0	498	AW545512	CO194F04-
711	15.2	76.0	498	AQ942565	Sheared D
712	15.2	76.0	500	BE588402	194027 BA
713	15.2	76.0	500	CB333785	STR00669
714	15.2	76.0	500	BZ218113	CH230-518
c 715	15.2	76.0	502	BM047404	RPCI-24-3
716	15.2	76.0	504	BW341166	BM341166
c 717	15.2	76.0	504	CG596203	OST257846
718	15.2	76.0	505	BM088054	501420 MA
719	15.2	76.0	505	BM221524	K0105H03-
c 720	15.2	76.0	506	BY465904	BY465904
c 721	15.2	76.0	508	AI716129	UI-R-Y0-a
722	15.2	76.0	509	AI854729	UI-M-BH0-
c 723	15.2	76.0	509	CF937809	CEST3e36
724	15.2	76.0	511	AA787508	nsf05a1.r
725	15.2	76.0	511	AA787508	nsf05a1.r
726	15.2	76.0	511	CB717258	AMGNNUC-N
c 727	15.2	76.0	513	AA739101	vv66e01.r
c 728	15.2	76.0	513	CB287895	CMD69_E07
729	15.2	76.0	514	AI326872	mJ55c08.x
c 730	15.2	76.0	514	BS551990	dae12a12.
c 731	15.2	76.0	517	BB759189	BB759189
c 732	15.2	76.0	518	AW021138	df19c09.y
c 733	15.2	76.0	518	CK949882	4075197 B
c 734	15.2	76.0	518	CR140881	reverse s
735	15.2	76.0	519	BM213215	C0833B11-
736	15.2	76.0	520	BI472274	fr99g10.y
737	15.2	76.0	522	BI472311	fs01d10.y
738	15.2	76.0	522	BI984471	fu03a03.y
739	15.2	76.0	524	BB283526	BB283526
c 740	15.2	76.0	524	BW384477	BW384477
741	15.2	76.0	528	AZ406627	IM0175M19
742	15.2	76.0	528	AL491345	T. brucei
743	15.2	76.0	530	BB693471	BB693471
744	15.2	76.0	532	AQ602813	HS 2132 A
745	15.2	76.0	533	CK940775	4064326 B
746	15.2	76.0	533	CK959797	4100756 B
747	15.2	76.0	533	AL473748	T. brucei
748	15.2	76.0	534	BO7924	pBAC 3.18 r
c 749	15.2	76.0	534	CE106719	tigr-gss-
c 750	15.2	76.0	535	AA032775	ml355f07.r

ALIGNMENTS

RESULT 1
BY283543
LOCUS
DEFINITION
BY283543
ACCESSION
BY283543
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

BY283543 RIKEN full-length enriched, visual cortex Mus musculus
CDNA clone K330012E08 5', mRNA sequence.
BY283543
BY283543.1 GI:26473880
EST.
Mus musculus (house mouse)
Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 423)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Oeato, N., Saito, R., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Kiyosawa, H., Yagi, K., Gojibori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bruscia, V.,
Choithia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shmida, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

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The Institute of Physical and Chemical Research (RIKEN)
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken

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FEATURES
Source
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    /organism="Homo sapiens"
    /mol_type="mRNA"
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    /cell_type="pre-B cell"
    /dev_stage="pediatric 2 years"
    /lab_host="DH10B"
    /clone_lib="Pediatric pre-B cell acute lymphoblastic
    leukemia Baylor-HGSC project=TCBA"
    /notes="vector: lambda PSB; Site_1: BamHI; Site_2: EcoRI;
    First strand cDNA was primed with an anchored
    3'oligo(dT) primer [5'GGAGGACTCGGCGCCGAGGAG(T)VN
    XhoI-oigo(C,G; N=A,C,G; T=A,C,G; T=A,C,G; T=A,C,G;
    was primed with a BamHI-dC primer
    [5'AGAGACTCGGATCGGCGCGCAATAAT(C) 3'].

```



```

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Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
Location/Qualifiers
1..497
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/tissue_type="ovary"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG9-ovary"
/note="Organ: ovary; Vector: Dog pBluescript LION"

FEATURES
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Query Match 100.0%; Score 20; DB 7; Length 497;
Best Local Similarity 80.0%; Pred. No. 99;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGAGCCUU 20
Db 352 AACGGAGCGCGGATGCCTT 333
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RESULT 7
LOCUS AY416380 500 bp DNA linear GSS 17-DEC-2003
DEFINITION Pan troglodytes BCL2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY416380
VERSION AY416380.1 GI:39772340
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 500)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 500)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
Location/Qualifiers
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
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gene
ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 500;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGAGCCUU 20

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Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
Location/Qualifiers
1..497
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/tissue_type="ovary"
/dev_stage="adult"
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/note="Organ: ovary; Vector: Dog pBluescript LION"

FEATURES
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Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGAGCCUU 20
Db 311 AACGGAGCGCGGATGCCTT 292
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RESULT 8
LOCUS CO624236 503 bp mRNA linear EST 22-JUL-2004
DEFINITION DG9-ovary Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO624236
VERSION CO624236.1 GI:50527466
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 503)
Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
Henrich, J. and Loebbert, R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schlueter
LION bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
Location/Qualifiers
1..536
/organism="Canis familiaris"

FEATURES
source
Query Match 100.0%; Score 20; DB 7; Length 536;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGAGCCUU 20
Db 311 AACGGAGCGCGGATGCCTT 292
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RESULT 9
LOCUS CO618349 536 bp mRNA linear EST 22-JUL-2004
DEFINITION DG9-185b3 DG9-ovary Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO618349
VERSION CO618349.1 GI:50521579
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 536)
Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
Henrich, J. and Loebbert, R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schlueter
LION bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
Location/Qualifiers
1..536
/organism="Canis familiaris"

FEATURES
source

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ORIGIN

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Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
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Db 354 AACGGAGGCTGGATGCCTT 335

RESULT 10
CO635169/c

LOCUS
DEFINITION DG9-99J1 DG9-ovary Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO635169
VERSION CO635169.1 GI:50538399
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
Henrich, J. and Loebbert, R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schlueter
LION bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.

FEATURES
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Location/Qualifiers
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ORIGIN

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Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
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Db 355 AACGGAGGCTGGATGCCTT 336

RESULT 11
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LOCUS
DEFINITION AL703462 602 bp mRNA linear EST 04-SEP-2003
KFZp686H0921.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
ACCESSION AL703462
VERSION AL703462.1 GI:19686917
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 602)
Ansoerge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)
EST (Ansoerge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No SI sequence available.
This clone (DKFZp686H0921) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clonerzpd.de.

FEATURES
source
Location/Qualifiers
1..602
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686H0921"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
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cDNA-collection"

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 602;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
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Db 138 AACGGAGGCTGGATGCCTT 157

RESULT 12
BF195698/c

LOCUS
DEFINITION BF195698 613 bp mRNA linear EST 03-NOV-2000
7n87C09.x1 NCI CGAP Ov18 Homo sapiens cDNA clone IMAGE:3571577 3',
similar to TR:O02718 O02718 BCL-2 ;, mRNA sequence.
ACCESSION BF195698
VERSION BF195698.1 GI:11082858
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 613)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.W.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
High quality sequence stop: 280.
Location/Qualifiers
1..613
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
 /clone="IMAGE:3571577"
 /tissue_type="fibrothecoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NCI_CGAP_Ov18"
 /note="Organ: ovary; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TTTTACCAATCTGAAGTGGAGCGCGCGACATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaudo."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 613;
 Best Local Similarity 80.0%; Pred. No.1e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AACGGAGCGUGGAGUGCCUU 20
 |||||:|||||:|||||:
 Db 270 AACGGAGCGTGGGATGCCTT 251
 |||||:|||||:|||||:

RESULT 13

CO708923/c
 LOCUS CO708923 627 bp mRNA linear EST 27-JUL-2004
 DEFINITION DG14-muscle Canis familiaris cDNA 3', mRNA sequence.

ACCESSION CO708923

VERSION CO708923.1 GI:50674469

KEYWORDS EST.

SOURCE Canis familiaris (dog)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE

1 (bases 1 to 627)
 Schluter, T., Hermans, J., Weindel, M., Schuette, D., Kranz, H.,
 Henrich, J., and Loebbert, R.

AUTHORS

Dog arrayTAG cDNA clone collection

TITLE

Unpublished (2004)

JOURNAL

Contact: Thomas Schluter

COMMENT

LION Bioscience AG
 Walldorferstrasse 98, D-69123 Heidelberg, Germany
 Tel: +49 6221 4038 150
 Fax: +49 6221 4038 290

Email: Thomas.Schluter@lionbioscience.com.

FEATURES

Location/Qualifiers

1..627
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /strain="Beagle"
 /db_xref="taxon:9615"
 /tissue_type="muscle"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="DG14-muscle"
 /note="Organ: muscle; Vector: Dog pBluescript LION"

ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 627;
 Best Local Similarity 80.0%; Pred. No.1e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AACGGAGCGUGGAGUGCCUU 20
 |||||:|||||:|||||:
 Db 355 AACGGAGCGTGGGATGCCTT 336
 |||||:|||||:|||||:

RESULT 14

BB409769
 LOCUS BB409769 685 bp mRNA linear EST 25-OCT-2001
 DEFINITION BB409769 FIKEN full-length enriched, 7 days embryo Mus musculus

cDNA clone C430015F12 3', mRNA sequence.

BB409769

VERSION BB409769.2 GI:16423206

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 685)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
 Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
 Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
 Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
 Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)

TITLE

JOURNAL

COMMENT

On Jul 15, 2000 this sequence version replaced gi:9229165.
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, Y., Hayata, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
 Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
 and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
 Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
 Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp/) for
 further details.

cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.

Location/Qualifiers
 1..685
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="C430015F12"
 /dev_stage="7 days embryo"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 7 days embryo"
 /note="Site 1: Sali; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTTTTTT 3'], cDNA was

FEATURES

source

prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATCTCGAGTTAATTAATTCCTCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 685;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 16; Conservative 4; Mismatches 0

QY 1 AACGGAGGCGUGGAGCCUU 20

|||||:|||||:|||||:|||||:
Db 303 AACGGAGGCTGGATGCCTT 322

RESULT 15

AY416381

LOCUS 711 bp DNA linear GSS 17-DEC-2003
DEFINITION Mus musculus BCL2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION

AY416381

VERSION

AY416381.1 GI:39772341

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

Location/Qualifiers

1..711

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

<1..>711

/gene="BCL2"

/locus_tag="HCM5871"

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 20; DB 9; Length 711;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20

|||||:|||||:|||||:|||||:
Db 565 AACGGAGGCTGGATGCCTT 584

RESULT 16

AY416379

LOCUS 720 bp DNA linear GSS 17-DEC-2003

DEFINITION Homo sapiens BCL2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION

AY416379

VERSION

AY416379.1 GI:39772339

KEYWORDS

SOURCE GSS

ORGANISM

Homo sapiens (human)

REFERENCE

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

Location/Qualifiers

1..720

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

<1..>720

/gene="BCL2"

/locus_tag="HCM5871"

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 20; DB 9; Length 720;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20

|||||:|||||:|||||:|||||:
Db 574 AACGGAGGCTGGATGCCTT 593

RESULT 17

BF448405/c

LOCUS

BF448405.1

DEFINITION

7n88c09.x1 NCI_CGAP Ov18 Homo sapiens cDNA clone IMAGE:3571600 3',

similar to SW:BCL2_HUMAN P10415 APOPTOSIS REGULATOR BCL-2. i, mRNA

sequence.

BF448405

BF448405.1 GI:11514201

EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 747)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento

Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL, send email to:

info@image.lnl.gov

-RNA was provided by Akira Nakagawara, Div. of Biochemistry, Chiba Cancer Center Research Institute, 666-2 Nipona, Chuoh-ku, Chiba, 260-8717 Japan, whose assistance we gratefully acknowledged."

ORIGIN

Query Match 92.0%; Score 18.4; DB 2; Length 492;
Best Local Similarity 75.0%; Pred. No. 5.7e+02;
Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
|||||:||||:||||:
DB 106 AACGGAGGCTGTGATGCCTT 125

RESULT 24
BM363392
LOCUS
DEFINITION BS320054B20E05 513 bp mRNA linear EST 10-JAN-2002
BS320054B20E05 5', mRNA sequence.
ACCESSION BM363392
VERSION
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 513)
AUTHORS Lewin,H.A., Soares,M.B., Pardinas,J., Liu,L. and Larson,J.H.
TITLE Subtracted Lewin Cattle Spleen ESTs
JOURNAL Unpublished (2002)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for Cattle EST sequencing was provided by the USDA National
Research Initiative, Project No. 98-35205-6644, and a grant from
the Japanese Ministry of Agriculture Fisheries and Forestry to
H.A. Lewin and J.E. Womack. Base-calling/Quality scores: PHRED form
Washington University Genome Center. Vector-trimming: Cross_Match
from Washington University Genome Center PHRAP suite. This sequence
is vector free and at least 200bp in length.
Insert Length: 513 Std Error: 0.00
Plate: BS320054B20 row: E column: 05
Seq primer: CGCCAGCTCGAAATTAACC
High quality sequence stop: 513.

FEATURES source

1. .513
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Angus"
/db_xref="taxon:9913"
/clone="BS320054B20E05"
/sex="female"
/dev_stage="Adult"
/clone_lib="Subtracted Lewin Cattle Spleen"
/note="Organ: Spleen; Vector: pBluescript SK(+/-); Site 1:
ECORI; Site 2: XhoI; This BS cDNA library was generated by
subtraction of the original non-normalized bovine spleen
library with 16,800 previously sequenced clones from a
bovine placenta cDNA library. The original library was
constructed as described by Band et al (2000), Genome
Research 10(9): 1359 -1368."

ORIGIN

Query Match 92.0%; Score 18.4; DB 4; Length 513;
Best Local Similarity 80.0%; Pred. No. 5.7e+02;
Matches 16; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
|||||:||||:||||:
DB 476 AACGGAGGCTGGACGCCTT 495

RESULT 25
BB771745
LOCUS
DEFINITION BB771745 RIKEN full-length enriched, B16 F10Y cells Mus musculus
cDNA clone G370137A02 3', mRNA sequence.
ACCESSION BB771745
VERSION
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM

REFERENCE 1 (bases 1 to 523)
AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-ree@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Kira,A.,
Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.

FEATURES source

1. .523
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G370137A02"
/cell_type="B16 F10Y cells"
/clone_lib="RIKEN full-length enriched, B16 F10Y cells"

ORIGIN

Query Match 92.0%; Score 18.4; DB 2; Length 523;
Best Local Similarity 75.0%; Pred. No. 5.7e+02;
Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 AACGGAGCGCGGGAUGCCUU 20
| |||||:||||:||||:
Db 147 ACGGAGCGCGGATGCCTT 166

RESULT 26
A1981239
LOCUS
DEFINITION pat.pk0049.b11.f chicken activated T cell cDNA Gallus gallus cDNA
clone pat.pk0049.b11.f 5' similar to bcl-2 protein, mRNA sequence.
ACCESSION A1981239
VERSION A1981239.1 GI:5884267
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 593)
Tirunagar,V.G., Sofer,L., Cui,J. and Burnside,J.
An expressed sequence tag database of T-cell-enriched activated
chicken splenocytes; sequence analysis of 5251 clones
Genomics 66 (2), 144-151 (2000)
20318616
10860659
Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1345
Fax: 302-831-3411
Email: joan@udel.edu, www.chickest.udel.edu
Seq primer: T7.
Location/Qualifiers
1..593
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pat.pk0049.b11.f"
/sex="male"
/cell_type="Con A-activated splenic T cell"
/lab_host="E.coli TOP10 F'"
/clone_lib="chicken activated T cell cDNA"
/note="Vector: pCDNA3"

FEATURES
source
Location/Qualifiers
1..593
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pat.pk0049.b11.f"
/sex="male"
/cell_type="Con A-activated splenic T cell"
/lab_host="E.coli TOP10 F'"
/clone_lib="chicken activated T cell cDNA"
/note="Vector: pCDNA3"

ORIGIN
Query Match 92.0%; Score 18.4; DB 1; Length 593;
Best Local Similarity 75.0%; Pred. No. 5.8e+02;
Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGGAUGCCUU 20
| |||||:||||:||||:
Db 8 ACGGAGCGCGGATGCCTT 27

RESULT 27
W16827/c
LOCUS
DEFINITION zblif01.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:301753 5', mRNA sequence.
ACCESSION W16827
VERSION W16827.1 GI:1291485
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 437)
Hillier,L., Clark,M., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 391.
Location/Qualifiers
1..437
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1246684"
/db_xref="taxon:9606"
/clone="IMAGE:301753"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_lung_NbHL19W"
/notes="Organ: lung; Vector: p7713D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; let
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGAGCGCGCAATTTTCTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7713 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W."

ORIGIN
Query Match 87.0%; Score 17.4; DB 7; Length 437;
Best Local Similarity 73.7%; Pred. No. 1.7e+03;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ACGGAGCGCGGGAUGCCUU 20
| |||||:||||:||||:
Db 365 ACGGAGCGCGGATGCCTT 347

RESULT 28
CV067685
LOCUS
DEFINITION Le.mx0.37f09 SP6 Little Skate Multiple Tissues, Normalized
Leucoraja erinacea cDNA clone Le.mx0.37f09 5' similar to pdb|IG5J|A
Chain A. Complex Of Bcl-Xl With Peptide From Bad. Score = 175 bits
(444), Expect = 5e-43, mRNA sequence.
CV067685
VERSION CV067685.1 GI:51530849
KEYWORDS EST.
SOURCE Leucoraja erinacea (little skate)
ORGANISM Leucoraja erinacea
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elaosobranchii; Squalia; Hypnosqualea; Pristioraja; Batoidae;
Rajiformes; Rajidae; Leucoraja.
1 (bases 1 to 627)
Towle,D.W. and Smith,C.M.
Expressed sequence tags in a normalized cDNA library prepared from
multiple tissues of adult little skate, Leucoraja erinacea
Unpublished (2004)
Contact: David W. Towle
Marine DNA Sequencing and Analysis Center
Mount Desert Island Biological Laboratory
Old Bar Harbor Road, Salsbury Cove, ME 04672 USA
Tel: 207-288-9880 x474
Fax: 207-288-2130
Email: dtowle@mdibl.org

```

Plate: 37 row: f column: 09
Seq primer: SP6
High quality sequence stop: 500.

FEATURES

source
1. .627
/organism="Leucoraja erinacea"
/mol_type="mRNA"
/db_xref="taxon:7782"
/clone="Le_mx0.37f09"
/tissue_type="Liver, kidney, brain, testis, ovary, gill, heart, spleen, rectal gland"
/dev_stage="Adult"
/clone_lib="Little Skate Multiple Tissues, Normalized"

/note="Vector: pCMV Sport 6.1; Total RNA samples were prepared individually from each tissue, checked for quality, then pooled for construction and normalized of cDNA library by Invitrogen. Plasmids were isolated and inserts end-sequenced by the Marine DNA Sequencing and Analysis Facility at Mount Desert Island Biological Laboratory. Traces were processed for submission to dbEST by trace2dbest software (Parkinson, Anthony and Blaxter, unpublished software)."

ORIGIN

Query Match 87.0%; Score 17.4; DB 7; Length 627;
Best Local Similarity 73.7%; Pred. No. 1.7e+03;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACGGAGCGUGGAGCCUU 20
|||||:|||||:|||||:
Db 471 ACGGCGCTGGGATGCCTT 489

RESULT 29

CV222414 665 bp mRNA linear EST 16-SEP-2004
LOCUS Le_mx0.60all SP6 Little Skate Multiple Tissues, Normalized
DEFINITION Leucoraja erinacea cDNA clone Le_mx0.60all 5' similar to pdb|IGSJ|A Chain A, Complex Of Bcl-Xl With Peptide From Bad. Score = 174 bits (440), Expect = 2e-42, mRNA sequence.

CV222414
CV222414.1 GI:52169394
EST.

SOURCE

Leucoraja erinacea (little skate)
Leucoraja erinacea
Leucoraja erinacea
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squalia; Hynostomalea; Pristigaster; Batoidae; Rajiformes; Rajidae; Leucoraja.

REFERENCE

1 (bases 1 to 665)
Towle,D.W. and Smith,C.M.
Expressed sequence tags in a normalized cDNA library prepared from multiple tissues of adult little skate, Leucoraja erinacea

JOURNAL

Unpublished (2004)
Contact: David W. Towle
Marine DNA Sequencing and Analysis Center
Mount Desert Island Biological Laboratory
Old Bar Harbor Road, Salsbury Cove, ME 04672 USA
Tel: 207-288-9880 x474

Fax: 207-288-2130

Email: dtowle@idbl.org

Plate: 60 row: a column: 11

Seq primer: SP6

High quality sequence stop: 519.

FEATURES

source
1. .665
/organism="Leucoraja erinacea"
/mol_type="mRNA"
/db_xref="taxon:7782"
/clone="Le_mx0.60all"
/tissue_type="Liver, kidney, brain, testis, ovary, gill, heart, spleen, rectal gland"
/dev_stage="Adult"
/clone_lib="Little Skate Multiple Tissues, Normalized"

/note="Vector: pCMV Sport 6.1; Total RNA samples were prepared individually from each tissue, checked for quality, then pooled for construction and normalized of cDNA library by Invitrogen. Plasmids were isolated and inserts end-sequenced by the Marine DNA Sequencing and Analysis Facility at Mount Desert Island Biological Laboratory. Traces were processed for submission to dbEST by trace2dbest software (Parkinson, Anthony and Blaxter, unpublished software)."

ORIGIN

Query Match 87.0%; Score 17.4; DB 7; Length 665;
Best Local Similarity 73.7%; Pred. No. 1.8e+03;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACGGAGCGUGGAGCCUU 20
|||||:|||||:|||||:
Db 450 ACGGCGCTGGGATGCCTT 468

RESULT 30

CV222414 892 bp mRNA linear EST 25-MAR-2004
LOCUS CK985413
DEFINITION VTEST8 Chicken pineal cDNA library Gallus gallus cDNA, mRNA sequence.

CV222414

CK985413

VERSION CK985413.1 GI:45567123

KEYWORDS EST

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 892).

REFERENCE Hartman,S.L., Geng,T.Y., Long,E.C., Wynn,J.E., Chong,N.W.,

Klein,D.C. and Smith,E.J.

Expressed sequence tags from a chicken pineal cDNA library

Unpublished (2004)

Contact: Smith EJ

Department of Animal and Poultry Sciences

Virginia Polytechnic Institute and State University

2250 Littleton Reaves Hall, Virginia Tech, Blacksburg, VA 24061, USA

Tel: 540 231 6797

Fax: 540 231 3010

Email: esmith@vt.edu

Seq primer: M13 Forward

Location/Qualifiers

1. .892

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="White Leghorn"

/db_xref="taxon:9031"

/tissue_type="pineal gland"

/dev_stage="10-11 day-old chick"

/clone_lib="Chicken pineal cDNA library"

ORIGIN

Query Match 87.0%; Score 17.4; DB 7; Length 892;
Best Local Similarity 78.9%; Pred. No. 1.8e+03;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGCGUGGAGCCU 19
|||||:|||||:|||||:
Db 273 AACGGAGCGGATGCCTT 291

RESULT 31

CV222414 366 bp mRNA linear EST 12-DEC-2002
LOCUS BY412675
DEFINITION BY412675 RIKEN full-length enriched, CRL-1722 L5178Y-R Mus musculus cDNA clone I730091H21 3', mRNA sequence.

CV222414

BY412675

ACCESSION BY412675

VERSION BY412675.1 GI:26642261

```

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

EST.
Mus musculus (house mouse)

Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 366)
Okazaki, I., Furuno, M., Kaekawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Haegawa, Y., Nogami, A.,
Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
Chotia, C., Corbani, L. E., Cousins, S., Dalia, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Griboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tonita, M.,
Verardo, R., Wagner, L., Wanlestedt, C., Wang, Y., Watanabe, Y.,
Welle, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayashizaki, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kigawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
Location/Qualifiers
1. .366
/organism="Mus musculus"

/mol_type="mRNA"
/strain="DBA/2"
/db_xref="taxon:10090"
/clone="I730091H21"
/cell_line="CRL-1722 L5178Y-R"
/clone_lib="RIKEN full-length enriched, CRL-1722 L5178Y-R"

ORIGIN
Query Match 85.0%; Score 17; DB 5; Length 366;
Best Local Similarity 82.4%; Pred. No. 2.5e+03;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGGAGGCGGGAUGCCU 19
Db 10 CGGAGGCTGGGATGCCT 26
|||||:|||||:
|||||:|||||:

RESULT 32
AQ095759 398 bp DNA linear GSS 27-AUG-1998
LOCUS
DEFINITION
HS_3013_B1_E01_T7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3013 Col=1 Row=J, genomic survey
sequence.
ACCESSION
AQ095759.1 GI:3463494
VERSION
AQ095759.1
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 398)
AUTHORS
Mahairas, G. G., Wallace, J. C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M. D. and
Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
1049764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3013 row: J column: 1
Class: BAC ends
High quality sequence stop: 398.
Location/Qualifiers
1. 398
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3013 Col=1 Row=J"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/notes="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

FEATURES
source
1. 398
Query Match 85.0%; Score 17; DB 8; Length 398;
Best Local Similarity 82.4%; Pred. No. 2.5e+03;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGGAGGCGGGAUGCCU 19
Db 277 CGGAGGCTGGGATGCCT 261
|||||:|||||:
|||||:|||||:

RESULT 33
AG583207/c

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LOCUS       AG583207               784 bp    DNA    linear    GSS 05-JUN-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-509123.T7, genomic survey
sequence.
ACCESSION   AG583207
VERSION     AG583207.1  GI:48344037
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus
ORGANISM    Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE       BAC end Sequences of Library MSMg01
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 784)
AUTHORS     Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY     : pBACe3.6
Vector      :
R.Site 1    : EcoRI.
R.Site 2    : EcoRI.
FEATURES    source
            1..784
                /organism="Mus musculus molossinus"
                /mol_type="genomic DNA"
                /sub_species="molossinus"
                /db_xref="taxon:57486"
                /clone="MSMg01-509123.T7"
                /sex="male"
                /tissue_type="mixture of kidney and spleen"
                /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN
Query Match      85.0%; Score 17; DB 9; Length 784;
Best Local Similarity 76.5%; Pred.No. 2.8e+03;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      4  GGAGGCTGGGAGCCUU 20
        |||||:||||:||||:
Db      457 GGAGGCTGGGATGCCTT 441

RESULT 34
CF113630
LOCUS       CF113630               252 bp    mRNA    linear    EST 23-JUL-2003
DEFINITION  Rattus norvegicus cDNA clone CP6958 5', mRNA sequence.
ACCESSION   CF113630
VERSION     CF113630.1  GI:33172725
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 252)
AUTHORS     Shultz,M.A., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B.,
            Plopper,C.G. and Buckpitt,A.R.

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TITLE       Gene expression analysis in response to lung toxicants: I.
            Sequencing and microarray development
JOURNAL     Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
COMMENT     Contact: Shultz MA
            Dept. of Molecular Biosciences, School of Veterinary Medicine
            University of California, Davis
            1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
            Tel: 530 752 0793
            Fax: 530 752 4698
            Email: mshultz@ucdavis.edu
            Average Phred score is 20 or better. All poor quality data (Phred <
            20) and vector/linker sequence has been removed.
            High quality sequence stop: 252.
FEATURES    Location/Qualifiers
            1..252
                /organism="Rattus norvegicus"
                /mol_type="mRNA"
                /strain="Sprague-Dawley"
                /db_xref="taxon:10116"
                /clone="CP6958"
                /sex="male"
                /tissue_type="airway or parenchyma"
                /dev_stage="adult"
                /clone_lib="Rat lung airway and parenchyma cDNA libraries"
                /note="Organ: lung; Vector: pGEM-11zf(-); Site.1: Eco RI;
            Site.2: Not I; mRNA was isolated from microdissected rat
            lung airways and parenchyma tissues."
ORIGIN
Query Match      84.0%; Score 16.8; DB 7; Length 252;
Best Local Similarity 70.0%; Pred.No. 3e+03;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1  AACGAGGCTGGGAGCCUU 20
        |||||:||||:||||:
Db      109 AAGGGCGCTGGGATGCCTT 128

RESULT 35
CG579617/c
LOCUS       CG579617               311 bp    mRNA    linear    GSS 02-OCT-2003
DEFINITION  OST218114 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST218114,
            mRNA sequence.
ACCESSION   CG579617
VERSION     CG579617.1  GI:37373605
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 311)
            Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.I.
            Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
            Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
            Contact: Zambrowicz BP
            OnniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES    Location/Qualifiers
            1..311
                /organism="Mus musculus"
                /mol_type="mRNA"

```



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/strain="129Sv/Ev"
/db_xref="taxon:10090"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
Query Match      84.0%; Score 16.8; DB 9; Length 311;
Best Local Similarity 70.0%; Pred. No. 3.1e+03;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy  1 AACGGAGGCTGGGAGGCCUU 20
    ||| |||||:||||:||||:
Db  101 AACTGAGGCTGGGATACCTT 82

RESULT 36
LOCUS      CD028860          355 bp      mRNA      linear      EST 07-MAY-2003
DEFINITION mgmy005x011.f Magnaporthe grisea MY Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgmy005x011 5', mRNA sequence.
ACCESSION  CD028860
VERSION     CD028860.1 GI:30410316
KEYWORDS   EST.
SOURCE     Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM   Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
REFERENCE  1 (bases 1 to 355)
AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
JOURNAL    Unpublished (2002)
COMMENT    Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person; Best nr hit (Apr 11, 22, 2003) sp|P06810|COX5_NEUCR
            Cytochrome c oxidase polypeptide V, mitocho. . . 123 5e-28
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgmy005 row: O column: 11
Seq primer: T3.

FEATURES             Location/Qualifiers
     source           1..355
     -                 /organism="Magnaporthe grisea"
     mol_type="mRNA"
     strain="70-15"
     db_xref="taxon:148305"
     clones="mgmy005x011"
     sex="Mat1-2 hermaphrodite"
     cell_type="mycelium"
     clone_lib="Magnaporthe grisea MY Uni-Zap XR Library"
     note="vector: phluescriptSK+; Site_1: EcoRI; Site 2:
     xhoI; Unidirectional cloning. EcoRI side has T3 primer and
     predominantly 5' reads. T7 primer on xhoI side of insert.
     Minimal medium mycelium library. Sequences were processed
     by one of two methods. Where a full-length alignment to
     the M. grisea genome sequence was available, the EST
     sequence was trimmed according to the alignment, otherwise
     sequence quality was assessed using phredphrap version
     991019 and trimmed according to phd files (0.05) and for
     vector seqs."

ORIGIN
Query Match      84.0%; Score 16.8; DB 6; Length 355;
Best Local Similarity 70.0%; Pred. No. 3.1e+03;

Qy  1 AACGGAGGCTGGGAGGCCUU 20
    ||| |||||:||||:||||:
Db  101 AACTGAGGCTGGGATACCTT 82

us-10-018-437-2.rst
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy  1 AACGGAGGCTGGGAGGCCUU 20
    ||| |||||:||||:||||:
Db  280 AAGGTAGGCTGGGATGCCTT 299

RESULT 37
LOCUS      BF544522          363 bp      mRNA      linear      EST 11-DEC-2000
DEFINITION UI-R-BT0-px-c-03-0-UI-r1 UI-R-BT0 Rattus norvegicus cDNA clone
            UI-R-BT0-px-c-03-0-UI 5', mRNA sequence.
ACCESSION  BF544522
VERSION     BF544522.1 GI:11635587
KEYWORDS   EST.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 363)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL    Genome Res. 6 (9), 791-806 (1996)
MEDLINE    97044477
PUBMED     8889548
COMMENT    Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            Clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LBNL (info@image.llnl.gov). IMAGE ID= 1788367
            Seq primer: M13 Forward.

FEATURES             Location/Qualifiers
     source           1..363
     -                 /organism="Rattus norvegicus"
     mol_type="mRNA"
     strain="Sprague-Dawley"
     db_xref="taxon:10116"
     clones="UI-R-BT0-px-c-03-0-UI"
     dev_stage="adult"
     lab_host="DH10B (Life Technologies)"
     clone_lib="UI-R-BT0"
     note="vector: pT7T3D-Pac (Pharmacia) with a modified
     polylinker; Site 1: Not I; Site 2: Eco RI; This library
     (UI-R-BT0) consists of a mixture of individually tagged
     normalized libraries constructed from rat hippocampus,
     thalamus, mid-brain, medulla, corpus striatum, cerebral
     cortex and testis. The tag used to identify the source
     tissue is a string of 3-6 nucleotides present
     between the
     Not I site and the oligo-dT track which allows
     identification of the library of origin of a clone within
     the mixture. This library was then subtracted using a
     driver consisting of a mixture of all clones from UI-R-A0,
     UI-R-A1, UI-R-E0, UI-R-E1, UI-R-C0, UI-R-C1, UI-R-C2 and
     UI-R-C2p."

ORIGIN
Query Match      84.0%; Score 16.9; DB 2; Length 363;
Best Local Similarity 70.0%; Pred. No. 3.1e+03;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy  1 AACGGAGGCTGGGAGGCCUU 20
    ||| |||||:||||:||||:
Db  344 AAGGGCGCTGGGATGCCTT 363

```

RESULT 38
BF554221/c
LOCUS
DEFINITION UI-R-C0-ho-h-02-0-UI-r1 UI-R-C0 Rattus norvegicus cDNA clone
UI-R-C0-ho-h-02-0-UI 5', mRNA sequence.
ACCESSION BF554221
VERSION BF554221.1 GI:11663951
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 382)
AUTHORS Bonaudo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1781719 The following
repetitive elements were found in this cDNA sequence: 213-273,
>PB1D10#SINE/Alu
Seq primer: M13 Forward.

FEATURES
source

Location/Qualifiers
1..382
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C0-ho-h-02-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-C0"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-C0
library is a subtracted library derived from the UI-R-A1
and UI-R-E1 libraries. The UI-R-A1 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, and muscle. The UI-R-E1
library consisted of a mixture of individually tagged
normalized libraries constructed from 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which
allows identification of the library of origin of a clone
within the mixture. The subtracted library (UI-R-C0) was
constructed as follows: PCR amplified cDNA inserts from a
pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had
been derived was used as a driver in a hybridization with
the pooled UI-R-A1 and UI-R-E1 library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-C0
library. This procedure has been previously described
(Bonaudo, Lennon and Soares, Genome Research 6: 791-806,
1996)"

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 382;
Best Local Similarity 70.0%; Pred. No. 3.2e+03;

Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AACGAGGCGUGGAGCCUU 20
Db |||||:||||:|:|:
99 AAGGGAGGCTGGGATACCTT 80
RESULT 39
BF1518513/c
LOCUS
DEFINITION 603061632F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211103 5',
mRNA sequence.
ACCESSION BF1518513
VERSION BF1518513.1 GI:15343305
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 396)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM11529 row: o column: 08
High quality sequence stop: 396.
Location/Qualifiers
1..396
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5211103"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH_MGC 118"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
ORIGIN
Query Match 84.0%; Score 16.8; DB 4; Length 396;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AACGAGGCGUGGAGCCUU 20
Db |||||:||||:|:|:
250 AGCGAGGCTGGGAGCCTT 231
RESULT 40
AA352879
LOCUS
DEFINITION AA352879 Activated T-cells XX Homo sapiens cDNA 5' end similar to
high mobility group protein 1, lymphocyte, mRNA sequence.
ACCESSION AA352879
VERSION AA352879.1 GI:2005270
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 452)

REFERENCE
AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Whi, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, E., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
96026280
7586098
Other ESTs: THCI189672
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
1. 452
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):153156"
/db_xref="taxon:9606"
/cell_type="T-lymphocyte"
/dev_stage="adult"
/clone_lib="Activated T-cells XX"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

FEATURES
source
1. 452

ORIGIN
Query Match 84.0%; Score 16.8; DB 1; Length 452;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGAGCCUU 20
|||||:||||:||||:
Db 345 AACGGAGCGCGGAGCCCTT 364

RESULT 41
R94119/c
LOCUS R94119
DEFINITION Yt74e06, rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:276179 5', mRNA sequence.
ACCESSION R94119
VERSION R94119.1 GI:969514
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

REFERENCE
AUTHORS Holman, M., Hultnan, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasaki, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1333
High quality sequence stops: 207
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1333 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 207.
Location/Qualifiers
1. 468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3799648"
/db_xref="taxon:9606"
/clone="IMAGE:276179"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_hosts="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACTGGAAGAATTAATAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 84.0%; Score 16.8; DB 7; Length 468;
Best Local Similarity 70.0%; Pred. No. 3.2e+03;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGAGCCUU 20
|||||:||||:||||:
Db 390 AACGGAGCGCGGAGCCCTT 371

RESULT 42
BU641963/c
LOCUS BU641963
DEFINITION mgmk010xE19f.b pmk1 in pBluescriptII sk(-) plasmid Magnaporthe grisea cDNA clone mgmk010xE19 5', mRNA sequence.
ACCESSION BU641963
VERSION BU641963.2 GI:30401625
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea) Magnaporthe grisea
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe. 1 (bases 1 to 471)
REFERENCE
AUTHORS Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Bhatte, K., and Dean, R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
Unpublished (2002)
On Sep 30, 2002 this sequence version replaced gi:23354290.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL MEDLINE
Nature 420. 563-573 (2002)

PUBMED
12466851

COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numasaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES source

```

1. 509
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="I530030J08"
/sex="female"
/tissue_type="placenta"
/dev_stage="12 days pregnant adult"
/clone_lib="RIKEN full-length enriched, 12 days pregnant adult female placenta"

```

ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 509;
Best Local Similarity 70.0%; Pred. No. 3.3e+03;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGGAUGCCUU 20
|||:|||||:|||||:|||||:
Db 373 AAGGAGCGCTGGGATTCCTT 354

RESULT 45

BM867198
LOCUS
mgcs009x009f.b Magnaporthe grisea CS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcs009x009 5', mRNA sequence.
ACCESSION
BM867198

VERSION BM867198.2 GI:30394042

KEYWORDS SOURCE ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 539)

REFERENCE

AUTHORS
Ebbols, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,
Bhatnagar, K. and Dean, R.A.

TITLE

Expressed sequence tags from the rice blast fungus, Magnaporthe grisea

JOURNAL

Unpublished (2002)

COMMENT

On Mar 7, 2002 this sequence version replaced gi:19234880.
Contact: Ebbols DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483

Email: d-ebbol@tamu.edu

Chromatogram file of this sequence is available, see contact person/Best nr hit (April. 22, 2003) sp|P06810|COX5_NEUCR

Cytochrome c oxidase polypeptide V, mitocho. . . 155 4e-37

PCR Primers

FORWARD: T3 primer

BACKWARD: T7 primer

Plate: mgcs009 row: 0 column: 09

Seq primer: T3.

Location/Qualifiers

1. .539

/organism="Magnaporthe grisea"

/mol_type="mRNA"

/strain="Guy11"

/db_xref="taxon:148305"

/clone="mgcs009x009"

/sex="Mat1-2 hermaphrodite"

/cell_type="conidia"

/clone_lib="Magnaporthe grisea CS Uni-Zap XR Library"

/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Conidial library. Point inoculation of Guy11 at center of oatmeal agar plate. Conidia were harvested after two weeks of growth. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredphrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Query Match 84.0%; Score 16.8; DB 4; Length 539;
Best Local Similarity 70.0%; Pred. No. 3.3e+03;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGGAUGCCUU 20
|||:|||||:|||||:|||||:
Db 321 AAGGTAGCTGGGATGCCTT 340

RESULT 46

CD031828
LOCUS
mgmt007xd12f.b Mated culture Magnaporthe grisea cDNA clone mgmt007xd12 5', mRNA sequence.
DEFINITION
CD031828
CD031828.1 GI:30413666

ACCESSION

VERSION
CD031828

KEYWORDS

SOURCE
Magnaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM

Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 545)

AUTHORS
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
Bhatterai,K. and Dean,R.A.
TITLE
Expressed sequence tags from the rice blast fungus, Magnaporthe
grisea
JOURNAL
Unpublished (2002)
COMMENT
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person;Best nr hit (April. 22, 2003) sp|P06810|COX5_NEUCR
Cytochrome c oxidase polypeptide V, mitocho. . . 162 2e-39
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgmt007 row: D column: 12
Seq primer: T3.
FEATURES
Location/Qualifiers
1..545
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="4091-5-8 X 4136-4-3"
/db_xref="taxon:148305"
/clone="mgmt007XD12"
/sex="Mat1-2 and Mat1-1 mixed culture"
/cell_type="mixed sexual development"
/dev_stage="asci, ascospores, perithecia, mycelium"
/clone_lib="Mated culture"
/notes="Vector: pBluescriptSK; Site 1: EcoRI; Site 2: XhoI;
Two mating types were co-cultivated over a filter-paper on
oatmeal agar medium. After three days at 25 C plates were
transferred to 21 C. Perithecia with asci and ascospores
collected by scraping tissue from the filter paper.
Sequences were processed by one of two methods. Where a
full-length alignment to the M. grisea genome sequence was
available, the EST sequence was trimmed according to the
alignment, otherwise sequence quality was assessed using
phredPhrap version 991019 and trimmed according to phd
files (0.05) and for vector seqs."
ORIGIN
Query Match 84.0%; Score 16.8; DB 6; Length 545;
Best Local Similarity 70.0%; Pred. No. 3.3e+03;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGGCCUU 20
|||:||||:||||:||||:
Db 339 AAGGTAGGCTGGGATGCTT 358

RESULT 47
BM866514 600 bp mRNA linear EST 06-MAY-2003
LOCUS mgc006xC01f.b Magnaporthe grisea CS Uni-Zap XR Library Magnaporthe
grisea cDNA clone mgc006xC01 5', mRNA sequence.
BM866514
ACCESSION BM866514.2 GI:30394631
VERSION
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 600)
REFERENCE
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe
grisea
JOURNAL Unpublished (2002)
COMMENT On Mar 7, 2002 this sequence version replaced gi:19234196.

Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person;Best nr hit (April. 22, 2003) sp|P06810|COX5_NEUCR
Cytochrome c oxidase polypeptide V, mitocho. . . 226 1e-58
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgc006 row: C column: 01
Seq primer: T3.
FEATURES
Location/Qualifiers
1..600
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgc006xC01"
/sex="Mat1-2 hermaphrodite"
/cell_type="conidia"
/clone_lib="Magnaporthe grisea CS Uni-Zap XR Library"
/note="Vector: pBluescriptSK; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Conidial library. Point inoculation of Guy11 at center of
oatmeal agar plate. Conidia were harvested after two weeks
of growth. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimmed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
ORIGIN
Query Match 84.0%; Score 16.8; DB 4; Length 600;
Best Local Similarity 70.0%; Pred. No. 3.3e+03;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGGCCUU 20
|||:||||:||||:||||:
Db 542 AAGGTAGGCTGGGATGCTT 561

RESULT 48
BQ391811/c 655 bp mRNA linear EST 22-MAY-2002
LOCUS NISC mg20h02.x1 NICHED XGC-Emb5 Xenopus tropicalis cDNA clone
DEFINITION IMAGE:5309043 3', mRNA sequence.
ACCESSION BQ391811
VERSION BQ391811.1 GI:21079498
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 655)
REFERENCE
AUTHORS NIH-XGC http://image.llnl.gov/image/html/xenopuslib.info.shtml.
National Institute of Child Health and Human Development, National
Cancer Institute, Xenopus Gene Collection
Unpublished (2002)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

info@image.llnl.gov
 Plate: L1AM11782 row: P column: 4
 Seq primer: -21M13 forward primer (AB1).

FEATURES

Source

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Xenopus Gene Collection (XGC) library."

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ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 655;
 Best Local Similarity 75.0%; Pred. No. 3.4e+03;
 Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGAGGCTGGGAGGCUU 20

Db 595 AACGAGGCTGGGAGGCTTT 576

RESULT 49
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LOCUS AG110319 670 bp DNA linear GSS 03-NOV-2001
 DEFINITION Pan troglodytes DNA, clone: PTB-116A04.F, genomic survey sequence.

ACCESSION AG110319

VERSION AG110319.1 GI:16730838

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

BAC end sequences of Library PTB

Unpublished

2 (bases 1 to 670)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: chimpanzee@gsc.riken.go.jp URL: http://hgp.gsc.riken.go.jp/.

Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the R&D process and may have higher chance of
 clone tracking errors.

PRIMERS

Sequencing: -21M13

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI.

Location/Qualifiers

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 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Db 668 AACGAGGCTGGGATGCTT 649

RESULT 50

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 DEFINITION tigr-gss-dog-17000333665743 Dog Library Canis familiaris genomic,
 genomic survey sequence.

ACCESSION CE276116

VERSION CE276116.1 GI:36019627

KEYWORDS GSS.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE

1 (bases 1 to 677)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,

Rusch, D.B., Delcher, A.L., Pop, M., Wang, M., Fraser, C.M. and

Venter, J.C.

The dog genome: survey sequencing and comparative analysis

Science 301 (5641), 1898-1903 (2003)

22875432

14513627

Contact: Kirkness EF

The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

Location/Qualifiers

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/mol_type="genomic DNA"

/strain="Standard Poodle"

/db_xref="taxon:9615"

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/notes="Site 1: BatXI; Libraries were prepared from

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 Best Local Similarity 70.0%; Pred. No. 3.4e+03;
 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGAGGCTGGGAGGCUU 20

Db 61 AACAGAGACTGGGATGCTT 42

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Job time : 3230 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 04:48:39 ; Search time 127 Seconds
(without alignments)
257.681 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacgagggcgggaugccuu 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 750 summaries

Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20	100.0	717	2	US-08-465-485A-20
5	20	100.0	717	3	US-09-080-285-20
6	20	100.0	760	1	US-08-405-702A-11
7	20	100.0	1846	2	US-08-365-486A-16
8	20	100.0	1846	3	US-08-880-342-16
9	20	100.0	4825	6	5459251-1
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12	20	100.0	5086	2	US-08-365-486A-14
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15	20	100.0	5086	3	US-09-724-426-19
16	20	100.0	5086	3	US-09-233-527-7
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18	20	100.0	5086	5	PCT-US93-06251-2
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68	15.2	76.0	735	2	US-08-464-134-118	Sequence 118, App
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C 251	14.2	71.0	1494	4	US-09-499-846-9	Sequence 9, Appl	C 324	14.2	71.0	11481	3	US-09-453-702B-25A	Sequence 25A, Appl
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C 253	14.2	71.0	1514	3	US-09-333-729A-2	Sequence 2, Appl	C 326	14.2	71.0	12460	4	US-09-949-016-13009	Sequence 13009, A
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C 255	14.2	71.0	1578	4	US-09-499-846-7	Sequence 7, Appl	C 328	14.2	71.0	13027	4	US-09-949-016-14361	Sequence 14361, A
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C 268	14.2	71.0	1796	3	US-08-485-372A-1	Sequence 1, Appl	C 341	14.2	71.0	35100	3	US-08-757-669A-19	Sequence 19, Appl
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C 288	14.2	71.0	2482	3	US-08-485-372A-3	Sequence 3, Appl	C 361	14.2	71.0	95109	4	US-09-949-016-16027	Sequence 16027, A
C 289	14.2	71.0	2482	3	US-09-409-006A-3	Sequence 3, Appl	C 362	14.2	71.0	95318	4	US-09-949-016-11784	Sequence 11784, A
C 290	14.2	71.0	2482	3	US-08-484-681-3	Sequence 3, Appl	C 363	14.2	71.0	95318	4	US-09-949-016-13938	Sequence 13938, A
C 291	14.2	71.0	2482	3	US-09-766-595-3	Sequence 3, Appl	C 364	14.2	71.0	106924	4	US-09-949-016-13934	Sequence 13934, A
C 292	14.2	71.0	2482	5	PCT-US93-07422-3	Sequence 3, Appl	C 365	14.2	71.0	116652	4	US-09-949-016-13413	Sequence 13413, A
C 293	14.2	71.0	2655	3	US-09-257-894-1	Sequence 1, Appl	C 366	14.2	71.0	121982	4	US-09-949-016-12085	Sequence 12085, A
C 294	14.2	71.0	2720	4	US-09-731-166-11	Sequence 11, Appl	C 367	14.2	71.0	121982	4	US-09-949-016-14105	Sequence 14105, A
C 295	14.2	71.0	2725	3	US-08-941-445A-14	Sequence 14, Appl	C 368	14.2	71.0	129899	4	US-09-949-016-14684	Sequence 14684, A
C 296	14.2	71.0	2816	1	US-08-785-241-1	Sequence 1, Appl	C 369	14.2	71.0	143644	4	US-09-949-016-15238	Sequence 15238, A
C 297	14.2	71.0	2818	3	US-09-374-454-7	Sequence 7, Appl	C 370	14.2	71.0	148156	4	US-09-949-016-11776	Sequence 11776, A
C 298	14.2	71.0	3192	4	US-09-949-016-2923	Sequence 2923, Appl	C 371	14.2	71.0	152481	4	US-09-949-016-12521	Sequence 12521, A
C 299	14.2	71.0	3441	4	US-09-270-767-14178	Sequence 14178, A	C 372	14.2	71.0	152481	4	US-09-949-016-12775	Sequence 12775, A
C 300	14.2	71.0	3489	4	US-09-949-016-2922	Sequence 2922, Appl	C 373	14.2	71.0	152822	4	US-09-949-016-17519	Sequence 17519, A
C 301	14.2	71.0	3663	4	US-09-715-962-3	Sequence 3, Appl	C 374	14.2	71.0	152822	4	US-09-949-016-12147	Sequence 12147, A
C 302	14.2	71.0	3968	4	US-09-270-767-12464	Sequence 12464, A	C 375	14.2	71.0	153643	4	US-09-949-016-12174	Sequence 12174, A
C 303	14.2	71.0	3975	4	US-09-270-767-3	Sequence 3, Appl	C 376	14.2	71.0	168174	4	US-09-949-016-15635	Sequence 15635, A
C 304	14.2	71.0	4464	4	US-09-485-473-5	Sequence 5, Appl	C 377	14.2	71.0	168174	4	US-10-071-411A-63	Sequence 63, Appl
C 305	14.2	71.0	4843	4	US-09-060-299-41	Sequence 41, Appl	C 378	14.2	71.0	168273	4	US-10-071-411A-2	Sequence 2, Appl
C 306	14.2	71.0	4843	4	US-09-402-923A-41	Sequence 41, Appl	C 379	14.2	71.0	187848	4	US-09-949-016-12111	Sequence 12111, A
C 307	14.2	71.0	5009	3	US-08-978-741-7	Sequence 7, Appl	C 380	14.2	71.0	221958	4	US-09-949-016-12173	Sequence 12173, A
C 308	14.2	71.0	5009	3	US-09-333-729A-8	Sequence 8, Appl	C 381	14.2	71.0	221966	4	US-09-949-016-15498	Sequence 15498, A
C 309	14.2	71.0	5117	4	US-09-060-299-40	Sequence 40, Appl	C 382	14.2	71.0	236964	4	US-09-949-016-15753	Sequence 15753, A
C 310	14.2	71.0	5117	4	US-09-402-923A-40	Sequence 40, Appl	C 383	14.2	71.0	250715	4	US-09-949-016-17394	Sequence 17394, A
C 311	14.2	71.0	5331	4	US-08-811-519-2	Sequence 2, Appl	C 384	14.2	71.0	301828	4	US-09-949-016-13969	Sequence 13969, A
C 312	14.2	71.0	5693	4	US-09-262-537-19	Sequence 19, Appl	C 385	14.2	71.0	767677	4	US-09-949-016-12147	Sequence 12147, A
C 313	14.2	71.0	5833	4	US-09-976-594-183	Sequence 183, Appl	C 386	14.2	71.0	767677	4	US-09-949-016-12147	Sequence 12147, A
C 314	14.2	71.0	6746	4	US-09-919-497-18	Sequence 18, Appl	C 387	14.2	71.0	767677	4	US-09-949-016-17361	Sequence 17361, A
C 315	14.2	71.0	6977	4	US-08-178-257-8	Sequence 8, Appl	C 388	14.2	71.0	767677	4	US-09-949-016-17361	Sequence 17361, A
C 316	14.2	71.0	7195	3	US-08-478-507-6	Sequence 6, Appl	C 389	14.2	71.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C 317	14.2	71.0	7195	3	US-09-128-275A-6	Sequence 6, Appl	C 390	14.2	71.0	441529	3	US-09-103-840A-1	Sequence 1, Appl
C 318	14.2	71.0	7195	3	US-09-553-427-6	Sequence 6, Appl	C 391	14.2	70.0	528	3	US-08-969-987-3	Sequence 3, Appl
C 319	14.2	71.0	7686	4	US-09-949-016-13489	Sequence 13489, A	C 392	14.2	70.0	601	4	US-09-949-016-79992	Sequence 79992, A
C 320	14.2	71.0	7686	4			C 393	14.2	70.0	601	4	US-09-949-016-152086	Sequence 152086, A

C 393	14	70.0	601	4	US-09-949-016-152159	Sequence 152159, App	466	13.8	69.0	458	4	US-09-270-767-9548	Sequence 9548, Ap
C 394	14	70.0	601	4	US-09-949-016-152232	Sequence 152232, App	467	13.8	69.0	458	4	US-09-270-767-24830	Sequence 24830, A
C 395	14	70.0	601	4	US-09-949-016-152305	Sequence 152305, App	468	13.8	69.0	462	4	US-09-107-433-1648	Sequence 1648, Ap
C 396	14	70.0	601	4	US-09-949-016-152391	Sequence 152391, App	469	13.8	69.0	485	3	US-09-085-199B-32	Sequence 32, Appl
C 397	14	70.0	601	4	US-09-949-016-152939	Sequence 152939, App	470	13.8	69.0	554	4	US-09-513-999C-3974	Sequence 3974, Ap
C 398	14	70.0	601	4	US-09-949-016-159464	Sequence 159464, App	471	13.8	69.0	564	4	US-08-252-991A-7062	Sequence 7062, Ap
C 399	14	70.0	601	4	US-09-949-016-159537	Sequence 159537, App	472	13.8	69.0	601	4	US-08-949-016-20624	Sequence 20624, A
C 400	14	70.0	601	4	US-09-949-016-159610	Sequence 159610, App	473	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 401	14	70.0	601	4	US-09-949-016-189100	Sequence 189100, App	474	13.8	69.0	601	4	US-09-949-016-25572	Sequence 25572, A
C 402	14	70.0	737	4	US-09-949-016-189101	Sequence 189101, App	475	13.8	69.0	601	4	US-09-949-016-38254	Sequence 38254, A
C 403	14	70.0	755	2	US-08-737-980-1	Sequence 874, App	476	13.8	69.0	601	4	US-09-949-016-42479	Sequence 42479, A
C 404	14	70.0	780	3	US-09-949-016-150555	Sequence 150555, App	477	13.8	69.0	601	4	US-09-949-016-50137	Sequence 50137, A
C 405	14	70.0	780	3	US-09-949-016-150555	Sequence 150555, App	478	13.8	69.0	601	4	US-09-949-016-50138	Sequence 50138, A
C 406	14	70.0	1322	4	US-09-270-767-14938	Sequence 14938, App	479	13.8	69.0	601	4	US-09-949-016-50522	Sequence 50522, A
C 407	14	70.0	1591	3	US-09-399-913-50	Sequence 50, Appl	480	13.8	69.0	601	4	US-09-949-016-50523	Sequence 50523, A
C 408	14	70.0	2118	4	US-09-350-614-50	Sequence 50, Appl	481	13.8	69.0	601	4	US-09-949-016-50524	Sequence 50524, A
C 409	14	70.0	2413	3	US-09-350-614-50	Sequence 50, Appl	482	13.8	69.0	601	4	US-09-949-016-55698	Sequence 55698, A
C 410	14	70.0	2413	3	US-09-350-614-50	Sequence 50, Appl	483	13.8	69.0	601	4	US-09-949-016-67155	Sequence 67155, A
C 411	14	70.0	2413	3	US-09-350-614-50	Sequence 50, Appl	484	13.8	69.0	601	4	US-09-949-016-67156	Sequence 67156, A
C 412	14	70.0	4800	4	US-09-949-016-150555	Sequence 150555, App	485	13.8	69.0	601	4	US-09-949-016-67157	Sequence 67157, A
C 413	14	70.0	18136	4	US-09-949-016-15126	Sequence 15126, App	486	13.8	69.0	601	4	US-09-949-016-68730	Sequence 68730, A
C 414	14	70.0	19376	4	US-09-949-016-15126	Sequence 15126, App	487	13.8	69.0	601	4	US-09-949-016-73578	Sequence 73578, A
C 415	14	70.0	53558	4	US-09-949-016-15198	Sequence 15198, App	488	13.8	69.0	601	4	US-09-949-016-80928	Sequence 80928, A
C 416	14	70.0	65966	4	US-09-949-016-16616	Sequence 16616, App	489	13.8	69.0	601	4	US-09-949-016-95215	Sequence 95215, A
C 417	14	70.0	70770	4	US-09-949-016-17152	Sequence 17152, App	490	13.8	69.0	601	4	US-09-949-016-95216	Sequence 95216, A
C 418	14	70.0	73757	4	US-09-949-016-16938	Sequence 16938, App	491	13.8	69.0	601	4	US-09-949-016-95393	Sequence 95393, A
C 419	14	70.0	75378	4	US-09-949-016-15369	Sequence 15369, App	492	13.8	69.0	601	4	US-09-949-016-95394	Sequence 95394, A
C 420	14	70.0	78846	4	US-09-949-016-17140	Sequence 17140, App	493	13.8	69.0	601	4	US-09-949-016-95571	Sequence 95571, A
C 421	14	70.0	78846	4	US-09-949-016-12396	Sequence 12396, App	494	13.8	69.0	601	4	US-09-949-016-95572	Sequence 95572, A
C 422	14	70.0	78846	4	US-09-949-016-12791	Sequence 12791, App	495	13.8	69.0	601	4	US-09-949-016-95749	Sequence 95749, A
C 423	14	70.0	78846	4	US-09-949-016-12792	Sequence 12792, App	496	13.8	69.0	601	4	US-09-949-016-95750	Sequence 95750, A
C 424	14	70.0	78850	4	US-09-949-016-12793	Sequence 12793, App	497	13.8	69.0	601	4	US-09-949-016-116914	Sequence 116914, A
C 425	14	70.0	78850	4	US-09-949-016-16013	Sequence 16013, App	498	13.8	69.0	601	4	US-09-949-016-116915	Sequence 116915, A
C 426	14	70.0	78850	4	US-09-949-016-16014	Sequence 16014, App	499	13.8	69.0	601	4	US-09-949-016-117767	Sequence 117767, A
C 427	14	70.0	78850	4	US-09-949-016-16015	Sequence 16015, App	500	13.8	69.0	601	4	US-09-949-016-118850	Sequence 118850, A
C 428	14	70.0	78850	4	US-09-949-016-16016	Sequence 16016, App	501	13.8	69.0	601	4	US-09-949-016-118851	Sequence 118851, A
C 429	14	70.0	78850	4	US-09-949-016-16201	Sequence 16201, App	502	13.8	69.0	601	4	US-09-949-016-118852	Sequence 118852, A
C 430	14	70.0	78850	4	US-09-949-016-16202	Sequence 16202, App	503	13.8	69.0	601	4	US-09-949-016-121141	Sequence 121141, A
C 431	14	70.0	78850	4	US-09-949-016-16203	Sequence 16203, App	504	13.8	69.0	601	4	US-09-949-016-121198	Sequence 121198, A
C 432	14	70.0	119981	4	US-09-949-016-16204	Sequence 16204, App	505	13.8	69.0	601	4	US-09-949-016-121199	Sequence 121199, A
C 433	14	70.0	119981	4	US-09-949-016-11844	Sequence 11844, App	506	13.8	69.0	601	4	US-09-949-016-121200	Sequence 121200, A
C 434	14	70.0	169998	3	US-09-949-016-13606	Sequence 13606, App	507	13.8	69.0	601	4	US-09-949-016-122400	Sequence 122400, A
C 435	14	70.0	173992	4	US-09-676-610B-24	Sequence 24, Appl	508	13.8	69.0	601	4	US-09-949-016-122401	Sequence 122401, A
C 436	14	70.0	197496	4	US-09-877-177A-10	Sequence 13779, App	509	13.8	69.0	601	4	US-09-949-016-138211	Sequence 138211, A
C 437	14	70.0	302604	4	US-09-949-016-14588	Sequence 14588, App	510	13.8	69.0	601	4	US-09-949-016-138212	Sequence 138212, A
C 438	14	70.0	302604	4	US-09-949-016-14589	Sequence 14589, App	511	13.8	69.0	601	4	US-09-949-016-138213	Sequence 138213, A
C 439	14	70.0	308362	4	US-09-949-016-17119	Sequence 17119, App	512	13.8	69.0	601	4	US-09-949-016-138957	Sequence 138957, A
C 440	14	70.0	374159	4	US-09-949-016-15868	Sequence 15868, App	513	13.8	69.0	601	4	US-09-949-016-140969	Sequence 140969, A
C 441	13.8	69.0	22	3	US-09-462-606-19	Sequence 13, Appl	514	13.8	69.0	601	4	US-09-949-016-143384	Sequence 143384, A
C 442	13.8	69.0	25	4	US-09-396-196G-24579	Sequence 24579, App	515	13.8	69.0	601	4	US-09-949-016-143555	Sequence 143555, A
C 443	13.8	69.0	25	4	US-09-396-196G-24580	Sequence 24580, App	516	13.8	69.0	601	4	US-09-949-016-151155	Sequence 151155, A
C 444	13.8	69.0	25	4	US-09-396-196G-24581	Sequence 24581, App	517	13.8	69.0	601	4	US-09-949-016-154577	Sequence 154577, A
C 445	13.8	69.0	25	4	US-09-396-196G-24582	Sequence 24582, App	518	13.8	69.0	601	4	US-09-949-016-154578	Sequence 154578, A
C 446	13.8	69.0	25	4	US-09-396-196G-24583	Sequence 24583, App	519	13.8	69.0	601	4	US-09-949-016-154579	Sequence 154579, A
C 447	13.8	69.0	245	4	US-09-621-976-17698	Sequence 17698, App	520	13.8	69.0	601	4	US-09-949-016-154580	Sequence 154580, A
C 448	13.8	69.0	249	4	US-09-621-976-17697	Sequence 17697, App	521	13.8	69.0	601	4	US-09-949-016-160022	Sequence 160022, A
C 449	13.8	69.0	249	4	US-09-621-976-17697	Sequence 17697, App	522	13.8	69.0	601	4	US-09-949-016-160023	Sequence 160023, A
C 450	13.8	69.0	253	4	US-09-902-540-2871	Sequence 2871, App	523	13.8	69.0	601	4	US-09-949-016-163489	Sequence 163489, A
C 451	13.8	69.0	292	4	US-09-513-999C-11994	Sequence 11994, App	524	13.8	69.0	601	4	US-09-949-016-163490	Sequence 163490, A
C 452	13.8	69.0	307	4	US-09-313-294A-6897	Sequence 6897, App	525	13.8	69.0	601	4	US-09-949-016-169637	Sequence 169637, A
C 453	13.8	69.0	343	4	US-09-621-976-11201	Sequence 11201, App	526	13.8	69.0	601	4	US-09-949-016-174027	Sequence 174027, A
C 454	13.8	69.0	392	4	US-09-640-211A-268	Sequence 174027, App	527	13.8	69.0	601	4	US-09-949-016-174157	Sequence 174157, A
C 455	13.8	69.0	396	4	US-09-621-976-17342	Sequence 17342, App	528	13.8	69.0	601	4	US-09-949-016-175641	Sequence 175641, A
C 456	13.8	69.0	396	4	US-09-640-173-164	Sequence 164, App	529	13.8	69.0	601	4	US-09-949-016-188534	Sequence 188534, A
C 457	13.8	69.0	396	4	US-09-713-550-164	Sequence 164, App	530	13.8	69.0	601	4	US-09-949-016-191508	Sequence 191508, A
C 458	13.8	69.0	396	4	US-09-825-294-164	Sequence 164, App	531	13.8	69.0	601	4	US-09-949-016-191509	Sequence 191509, A
C 459	13.8	69.0	418	4	US-09-970-966-164	Sequence 164, App	532	13.8	69.0	601	4	US-09-949-016-191686	Sequence 191686, A
C 460	13.8	69.0	418	4	US-09-824-629-1	Sequence 1, Appl	533	13.8	69.0	601	4	US-09-949-016-191687	Sequence 191687, A
C 461	13.8	69.0	418	4	US-09-824-629-2	Sequence 2, Appl	534	13.8	69.0	601	4		
C 462	13.8	69.0	443	3	US-09-404-879A-278	Sequence 278, App	535	13.8	69.0	601	4		
C 463	13.8	69.0	443	4	US-09-338-333-278	Sequence 278, App	536	13.8	69.0	601	4		
C 464	13.8	69.0	443	4	US-09-215-681-278	Sequence 278, App	537	13.8	69.0	601	4		
C 465	13.8	69.0	443	4	US-09-216-003A-278	Sequence 278, App	538	13.8	69.0	601	4		
					US-09-667-857-278	Sequence 278, App	539	13.8	69.0	601	4		

539	13.8	69.0	601	4	US-09-949-016-191864	Sequence 191864,	c 612	13.8	69.0	2648	2	US-08-836-443-1	Sequence 1, Appll
540	13.8	69.0	601	4	US-09-949-016-191865	Sequence 191865,	c 613	13.8	69.0	2697	4	US-09-252-991A-7118	Sequence 7118, Ap
541	13.8	69.0	601	4	US-09-949-016-192042	Sequence 192042,	c 614	13.8	69.0	2739	4	US-09-902-540-9021	Sequence 9021, Ap
542	13.8	69.0	601	4	US-09-949-016-192043	Sequence 192043,	c 615	13.8	69.0	2911	3	US-09-171-710-1	Sequence 1, Appll
543	13.8	69.0	601	4	US-09-949-016-193944	Sequence 193944,	c 616	13.8	69.0	2976	4	US-09-949-016-5358	Sequence 5358, Ap
544	13.8	69.0	601	4	US-09-949-016-195320	Sequence 195320,	c 617	13.8	69.0	3017	1	US-08-444-792-1	Sequence 1, Appll
545	13.8	69.0	601	4	US-09-949-016-198997	Sequence 198997,	c 618	13.8	69.0	3017	1	US-08-445-042-1	Sequence 1, Appll
546	13.8	69.0	601	4	US-09-949-016-198998	Sequence 198998,	c 619	13.8	69.0	3065	3	US-09-171-710-3	Sequence 3, Appll
547	13.8	69.0	601	4	US-09-949-016-200183	Sequence 200183,	c 620	13.8	69.0	3172	6	5196511-1	Patent No. 5196511
548	13.8	69.0	601	4	US-09-949-016-200184	Sequence 200184,	c 621	13.8	69.0	3172	6	5196511-1	Patent No. 5196511
549	13.8	69.0	601	4	US-09-949-016-202563	Sequence 202563,	c 622	13.8	69.0	3245	1	US-07-935-311A-3	Sequence 3, Appll
550	13.8	69.0	612	4	US-09-949-016-202563	Sequence 394, App	c 623	13.8	69.0	3245	1	US-08-368-079-3	Sequence 3, Appll
551	13.8	69.0	614	3	US-08-998-416-861	Sequence 861, App	c 624	13.8	69.0	3245	5	PCI-US93-07996-3	Sequence 3, Appll
552	13.8	69.0	615	4	US-09-513-999C-247	Sequence 247, App	c 625	13.8	69.0	3261	4	US-09-949-016-2391	Sequence 2391, Ap
553	13.8	69.0	633	4	US-09-583-110-2558	Sequence 2558, Ap	c 626	13.8	69.0	3291	4	US-09-252-991A-2757	Sequence 2757, Ap
554	13.8	69.0	660	4	US-09-621-976-2394	Sequence 2394, Ap	c 627	13.8	69.0	3303	3	US-09-409-648-5	Sequence 5, Appll
555	13.8	69.0	705	4	US-09-614-912-185	Sequence 185, App	c 628	13.8	69.0	3303	3	US-09-409-648-6	Sequence 6, Appll
556	13.8	69.0	721	4	US-09-270-767-13366	Sequence 13366, A	c 629	13.8	69.0	3303	4	US-09-054-272-9	Sequence 9, Appll
557	13.8	69.0	759	4	US-09-513-999C-2310	Sequence 2310, Ap	c 630	13.8	69.0	3311	2	US-08-239-278-10	Sequence 10, Appl
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ALIGNMENTS

; Patent No. 5506344
; APPLICANT: TSUJIMOTO, YOSHIHIDE;CROCE, CARLO A.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR BCL-2GENE PRODUCT
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,193
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 228,704
; FILING DATE: 18-APR-1994
; APPLICATION NUMBER: 994,941
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: 663,010
; FILING DATE: 19-MAR-1991
; APPLICATION NUMBER: 883,687
; FILING DATE: 09-JUL-1986
; SEQ ID NO:3:
; LENGTH: 623
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RESULT 2
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; Patent No. 5506344
; APPLICANT: TSUJIMOTO, YOSHIHIDE;CROCE, CARLO A.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR BCL-2GENE PRODUCT
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,193
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 228,704
; FILING DATE: 18-APR-1994
; APPLICATION NUMBER: 994,941
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: 663,010
; FILING DATE: 19-MAR-1991
; APPLICATION NUMBER: 883,687
; FILING DATE: 09-JUL-1986
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Query Match 100.0%; Score 20; DB 6; Length 623;
Best Local Similarity 80.0%; Pred.No. 2.1;
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RESULT 3
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; Sequence 1, Application US/09741238
; Patent No. 6706867
; GENERAL INFORMATION:
; APPLICANT: Lorenz, Matthias
; TITLE OF INVENTION: DNA Array Sequence Selection
; Patent No. 6706867
; FILE REFERENCE: NIH-05076
; CURRENT APPLICATION NUMBER: US/09/741,238
; CURRENT FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0


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; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 20:
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; Patent No. 6040181
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; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; APPLICATION NUMBER: US 08/465,485
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; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 20:
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; LENGTH: 717 base pairs
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US-09-080-285-20

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RESULT 6
US-08-405-702A-11
; Sequence 11, Application US/08405702A
; Patent No. 5789389
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/ GENERAL INFORMATION:
/ APPLICANT: Tarasewicz, Dariusz G
/ APPLICANT: Schott, Brigitte
/ APPLICANT: Holzmayer, Tatiana A.
/ APPLICANT: Roninson, Igor B.
/ TITLE OF INVENTION: BCL2 Derived Genetic Elements Associated
/ TITLE OF INVENTION: with Sensitivity to Chemotherapeutic Drugs
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Banner & Witcoff, Ltd.
/ STREET: 10 South Wacker Drive, Suite 3000
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/405,702A
/ FILING DATE: 17-MAR-1995
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5789389nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 95,332
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-715-1000
/ TELEFAX: 312-715-1234
/ TELEX: 910-221-5317
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 760 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 21..740
/
US-08-405-702A-11

Query Match 100.0%; Score 20; DB 1; Length 760;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGAGCCUU 20
Db 594 AACGGAGCGTGGGATGCCTT 613

RESULT 7
US-08-365-486A-16
/ Sequence 16, Application US/08365486A
/ Patent No. 5834306
/ GENERAL INFORMATION:
/ APPLICANT: Webster, Keith A.
/ APPLICANT: Bishopric, Nanette H.
/ TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
/ TITLE OF INVENTION: Therapeutic Constructs
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dehlinger & Associates
/ STREET: 350 Cambridge Avenue, Suite 250
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/880,342
/ FILING DATE: 23-JUN-1997
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/IB95/00996
/ FILING DATE: 13-NOV-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/365,486
```

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/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/365,486A
/ FILING DATE: 23-DEC-1994
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sholtz, Charles K.
/ REGISTRATION NUMBER: 38,615
/ REFERENCE/DOCKET NUMBER: 8255-0018
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
/ TELEFAX: (415) 324-0960
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1846 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: bcl-2 fusion gene; Seto, et al.,
/ INDIVIDUAL ISOLATE: EMBO J 7:123 (1988)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 887..1606
/
US-08-365-486A-16

Query Match 100.0%; Score 20; DB 2; Length 1846;
Best Local Similarity 80.0%; Pred. No. 2.3;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGAGCCUU 20
Db 1460 AACGGAGCGTGGGATGCCTT 1479

RESULT 8
US-08-880-342-16
/ Sequence 16, Application US/08880342
/ Patent No. 6218179
/ GENERAL INFORMATION:
/ APPLICANT: Webster, Keith A.
/ APPLICANT: Bishopric, Nanette H.
/ APPLICANT: Murphy, Brian
/ APPLICANT: Laderoute, Keith R.
/ APPLICANT: Green, Christopher J.
/ TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
/ TITLE OF INVENTION: Therapeutic Constructs
/ NUMBER OF SEQUENCES: 37
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dehlinger & Associates
/ STREET: 350 Cambridge Avenue, Suite 250
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/880,342
/ FILING DATE: 23-JUN-1997
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/IB95/00996
/ FILING DATE: 13-NOV-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/365,486
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; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1846 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: bcl-2 fusion gene; Seto, et al.,
; INDIVIDUAL ISOLATE: EMBO J 7:123 (1988)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 887..1606
; US-08-880-342-16

Query Match 100.0%; Score 20; DB 3; Length 1846;
Best Local Similarity 80.0%; Pred. No. 2.3;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
Db 1460 AACGGAGGCTGGGATGCCCT 1479

RESULT 9
5459251-1
; Patent No. 5459251
; APPLICANT: Tsujimoto, Yoshida; Croce, Carlo A.
; TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
; SEQUENCES
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,704
; FILING DATE: 18-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 994,941
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: 663,010
; FILING DATE: 19-MAR-1991
; APPLICATION NUMBER: 883,687
; FILING DATE: 09-JUL-1986
; SEQ ID NO: 1:
; LENGTH: 4825
5459251-1

Query Match 100.0%; Score 20; DB 6; Length 4825;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
Db 2032 AACGGAGGCTGGGATGCCCT 2051

RESULT 10
5459251-1
; Patent No. 5459251
; APPLICANT: Tsujimoto, Yoshida; Croce, Carlo A.
; TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
; SEQUENCES
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,704
```

```
; FILING DATE: 18-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 994,941
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: 663,010
; FILING DATE: 19-MAR-1991
; APPLICATION NUMBER: 883,687
; FILING DATE: 09-JUL-1986
; SEQ ID NO: 1:
; LENGTH: 4825
5459251-1

Query Match 100.0%; Score 20; DB 6; Length 4825;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
Db 2032 AACGGAGGCTGGGATGCCCT 2051

RESULT 11
US-08-465-485A-19
; Sequence 19, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5086 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-465-485A-19

Query Match 100.0%; Score 20; DB 2; Length 5086;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AACGGAGGCGGGAUGCCUU 20
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 Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 12

US-08-365-486A-14
 ; Sequence 14, Application US/08365486A
 ; Patent No. 5834306
 ; GENERAL INFORMATION:
 ; APPLICANT: Webster, Keith A.
 ; APPLICANT: Bishopric, Nanette H.
 ; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 ; TITLE OF INVENTION: Therapeutic Constructs
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/365,486A
 ; FILING DATE: 23-DEC-1994
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sholtz, Charles K.
 ; REGISTRATION NUMBER: 38,615
 ; REFERENCE/DOCKET NUMBER: 8255-0018
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5086 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: human bcl-2 cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1459..2178
 ; US-08-365-486A-14

Query Match 100.0%; Score 20; DB 2; Length 5086;
 Best Local Similarity 80.0%; Pred. NO. 2.5;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20
 |||||:||||:|:
 Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 13

US-09-080-285-19
 ; Sequence 19, Application US/09080285
 ; Patent No. 6040181
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John
 ; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/080,285
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/465,485
 ; FILING DATE: 05-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/124,256
 ; FILING DATE: 20-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/840,716
 ; FILING DATE: 21-FEB-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/288,692
 ; FILING DATE: 22-DEC-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fortney, Andrew D.
 ; REGISTRATION NUMBER: 34,600
 ; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (408) 436-2070
 ; TELEFAX: (408) 436-2075
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5086 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-080-285-19

Query Match 100.0%; Score 20; DB 3; Length 5086;
 Best Local Similarity 80.0%; Pred. NO. 2.5;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20
 |||||:||||:|:
 Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 14
 US-08-880-342-14
 ; Sequence 14, Application US/08880342
 ; Patent No. 6218179
 ; GENERAL INFORMATION:
 ; APPLICANT: Webster, Keith A.
 ; APPLICANT: Bishopric, Nanette H.
 ; APPLICANT: Murphy, Brian
 ; APPLICANT: Laderoute, Keith R.
 ; APPLICANT: Green, Christopher J.
 ; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 ; TITLE OF INVENTION: Therapeutic Constructs
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5086 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: human bcl-2 cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1459..2178
; US-08-880-342-14

Query Match 100.0%; Score 20; DB 3; Length 5086;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGGCCUU 20
DB 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 15
US-09-724-426-19
; Sequence 19, Application US/09724426
; Patent No. 6414134
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
; FILE REFERENCE: 10412-024
; CURRENT APPLICATION NUMBER: US/09/724,426
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 19
; LENGTH: 5086
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-426-19

Query Match 100.0%; Score 20; DB 3; Length 5086;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGGCCUU 20
DB 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 16
US-09-233-527-7
; Sequence 7, Application US/09233527
; Patent No. 645617
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE REFERENCE: 01997/201004
; CURRENT APPLICATION NUMBER: US/09/233,527
; CURRENT FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 5086
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1459)...(2178)
US-09-233-527-7

Query Match 100.0%; Score 20; DB 3; Length 5086;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGGCCUU 20
DB 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 17
PCT-US93-05651-4
; Sequence 4, Application PC/TUS9305651
; GENERAL INFORMATION:
; TITLE OF INVENTION: A Gene Which Prevents Programmed Cell Death
; NUMBER OF SEQUENCES: 5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05651
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5086 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1459..2178
; OTHER INFORMATION: /product= "Bcl-2"
PCT-US93-05651-4

Query Match 100.0%; Score 20; DB 5; Length 5086;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGGCCUU 20
DB 2032 AACGGAGGCTGGGATGCCTT 2051
```

```
RESULT 18
PCT-US93-06251-2
; Sequence 2, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5086 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-2
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```
Query Match 100.0%; Score 20; DB 5; Length 5086;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20
|||||:|||||:|||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051
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RESULT 19
US-09-234-186-7
; Sequence 7, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 7
; LENGTH: 5086
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1459)...(2178)
US-09-234-186-7
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Query Match 100.0%; Score 20; DB 3; Length 5094;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AACGGAGGCGGGAUGCCUU 20
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Db 2032 AACGGAGGCTGGGATGCCTT 2051
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RESULT 20
5506344-1
; Patent No. 5506344
; APPLICANT: TSUJIMOTO, YOSHIHIDE;CROCE, CARLO A.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR BCL-2GENE PRODUCT
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,193
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 228,704
; FILING DATE: 18-APR-1994
; APPLICATION NUMBER: 994,941
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: 663,010
; FILING DATE: 19-MAR-1991
; APPLICATION NUMBER: 883,687
; FILING DATE: 09-JUL-1986
; SEQ ID NO:1:
; LENGTH: 5104
5506344-1
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Query Match 100.0%; Score 20; DB 6; Length 5104;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20
|||||:|||||:|||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051
```

```
RESULT 21
5506344-1
; Patent No. 5506344
; APPLICANT: TSUJIMOTO, YOSHIHIDE;CROCE, CARLO A.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR BCL-2GENE PRODUCT
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,193
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 228,704
; FILING DATE: 18-APR-1994
; APPLICATION NUMBER: 994,941
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: 663,010
; FILING DATE: 19-MAR-1991
; APPLICATION NUMBER: 883,687
; FILING DATE: 09-JUL-1986
; SEQ ID NO:1:
; LENGTH: 5104
5506344-1
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```
Query Match 100.0%; Score 20; DB 6; Length 5104;
Best Local Similarity 80.0%; Pred. No. 2.5;
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Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAUGCCUU 20
 Db 2032 AACGGAGGCTGGGATGCTT 2051

RESULT 22

US-09-023-655-1015
 ; Sequence 1015, Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Susan G. Stuart
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 ; TITLE OF INVENTION: EXPRESSION
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023,655
 FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1015:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6030 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: gl79370
 US-09-023-655-1015

Query Match 100.0%; Score 20; DB 4; Length 6030;
 Best Local Similarity 80.0%; Pred. No. 2.5;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAUGCCUU 20
 Db 605 AACGGAGGCTGGGATGCTT 624

RESULT 23

US-09-023-655-432/c
 ; Sequence 432, Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Susan G. Stuart
 ; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 ; TITLE OF INVENTION: EXPRESSION
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023,655
 FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 432:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 379 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: BMARNOT03
 CLONE: 1668184
 US-09-023-655-432

Query Match 84.0%; Score 16.8; DB 4; Length 379;
 Best Local Similarity 75.0%; Pred. No. 72;
 Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAUGCCUU 20
 Db 326 AGCGGAGGCTGGGAGCCTT 307

RESULT 24

US-09-484-9708-31/c
 ; Sequence 31, Application US/094849708
 ; Patent No. 6426186
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Karen A.
 ; APPLICANT: Volkmuth, Wayne
 ; APPLICANT: Walker, Michael G.
 ; TITLE OF INVENTION: BONE REMODELING GENES
 ; FILE REFERENCE: PB-0014 US
 ; CURRENT APPLICATION NUMBER: US/09/484,970B
 ; CURRENT FILING DATE: 2000-01-18
 ; NUMBER OF SEQ ID NOS: 172
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 31
 ; LENGTH: 950
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. 6426186 236378.4CBI
 ; NAME/KEY: unsure
 ; LOCATION: 318, 353, 718

```
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-31

Query Match      84.0%; Score 16.8; DB 3; Length 950;
Best Local Similarity 75.0%; Pred.No. 78;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAGCCUU 20
Db 897 AGCGAGGCTGGAGGCCTT 878

RESULT 25
US-09-774-528-333/c
; Sequence 333, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aйдong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NO. 6743619el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 333
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1068)
US-09-774-528-333

Query Match      84.0%; Score 16.8; DB 4; Length 1154;
Best Local Similarity 70.0%; Pred.No. 79;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAGCCUU 20
Db 130 AAAGGAGTCTGGAGTCCTT 111

RESULT 26
US-09-949-016-15639
; Sequence 15639, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; OTHER INFORMATION: a, t, c, g, or other
US-09-949-016-15639

Query Match      84.0%; Score 16.8; DB 4; Length 112112;
Best Local Similarity 70.0%; Pred.No. 1.2e+02;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAGCCUU 20
Db 11785 AATGGAGGCTGAGATGCCTT 11804

RESULT 27
US-09-949-016-12777/c
; Sequence 12777, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12777
; LENGTH: 828152
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(828152)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12777

Query Match      80.0%; Score 16; DB 4; Length 828152;
Best Local Similarity 81.2%; Pred.No. 3.2e+02;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGAGGCGUGGAGCCUU 19
Db 815056 GGAGGCTGGATGCCT 815041

RESULT 28
US-09-949-016-20682
; Sequence 20682, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012
```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20682
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-20682

Query Match 79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 73.7%; Pred. No. 2.3e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAUGCCU 19
| ||||| : ||| : ||| :
Db 112 ACCGAGGCTGGGGTGCCCT 130

RESULT 29

US-09-949-016-20683
; Sequence 20683, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20683
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-20683

Query Match 79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 73.7%; Pred. No. 2.3e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAUGCCU 19
| ||||| : ||| : ||| :
Db 176 ACCGAGGCTGGGGTGCCCT 194

RESULT 30

US-09-949-016-20684
; Sequence 20684, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20684
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human

US-09-949-016-20684

Query Match 79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 73.7%; Pred. No. 2.3e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAUGCCU 19
| ||||| : ||| : ||| :
Db 196 ACCGAGGCTGGGGTGCCCT 214

RESULT 31

US-09-949-016-20685
; Sequence 20685, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20685
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-20685

Query Match 79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 73.7%; Pred. No. 2.3e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAUGCCU 19
| ||||| : ||| : ||| :
Db 356 ACCGAGGCTGGGGTGCCCT 374

RESULT 32

US-09-949-016-128302/c
; Sequence 128302, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128302
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-128302

Query Match 79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 68.4%; Pred. No. 2.3e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGAGGCUGGGAUGCCUU 20
||| ||| : || : :
Db 128 ACGAGGCTGGGCTGCATT 110

```

RESULT 33
US-09-949-016-194506/c
; Sequence 194506, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194506
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-194506

```

```

RESULT 34
US-09-949-016-194507/c
; Sequence 194507, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194507
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-194507

```

```

RESULT 35
US-09-949-016-202189
; Sequence 202189, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202189
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-202189

```

```

RESULT 36
US-09-949-016-202190
; Sequence 202190, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202190
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-202190

```

RESULT 37
US-09-949-016-202191
; Sequence 202191, Application US/09949016
; Patent No. 6812339


```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202191
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-202191

Query Match          79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 73.7%; Pred. No. 2.3e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCU 19
| | | | | | | | | | | | | | | | | | | | | |
Db 196 ACCGGAGGCTGGGGTGCT 214

RESULT 38
US-09-949-016-202192
; Sequence 202192, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202192
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-202192

Query Match          79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 73.7%; Pred. No. 2.3e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCU 19
| | | | | | | | | | | | | | | | | | | | | |
Db 356 ACCGGAGGCTGGGGTGCT 374

RESULT 39
US-09-968-362A-17/c
; Sequence 17, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
```

```
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vPc gamma2 (Figure 2A)
US-09-968-362A-17

Query Match          79.0%; Score 15.8; DB 4; Length 1368;
Best Local Similarity 73.7%; Pred. No. 2.5e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACCGAGGCGUGGAUGCCU 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1013 ATGGAGGCTGGGAGGCCTT 995

RESULT 40
US-09-949-016-17413/c
; Sequence 17413, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17413
; LENGTH: 15507
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17413

Query Match          79.0%; Score 15.8; DB 4; Length 15507;
Best Local Similarity 73.7%; Pred. No. 3.1e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCU 19
| | | | | | | | | | | | | | | | | | | | | |
Db 12912 ACCGGAGGCTGGGGTGCT 12894

RESULT 41
US-09-949-016-11891/c
; Sequence 11891, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11891
; LENGTH: 15511
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11891

Query Match          79.0%; Score 15.8; DB 4; Length 15511;
Best Local Similarity 73.7%; Pred. No. 3.1e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCU 19
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Db 12912 ACCGGAGGCTGGGTCCT 12894

RESULT 42
US-09-949-016-13153
; Sequence 13153, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13153
; LENGTH: 25230
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13153

Query Match          79.0%; Score 15.8; DB 4; Length 25230;
Best Local Similarity 68.4%; Pred. No. 3.2e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACCGAGGCGUGGAUGCCU 20
    |||||:||||:|:|:|:
Db 2703 ACCGAGCTGGGATGCTT 2721

RESULT 43
US-09-949-016-15378
; Sequence 15378, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15378
; LENGTH: 83516
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15378

Query Match          79.0%; Score 15.8; DB 4; Length 83516;
Best Local Similarity 68.4%; Pred. No. 3.5e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACCGAGGCGUGGAUGCCU 20
    |||||:||||:|:|:|:
Db 7978 ACCGAGGCTGGGTCATT 7996

RESULT 44
US-09-949-016-12160/c
; Sequence 12160, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12160
; LENGTH: 119032
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)_(119032)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-12160

Query Match          79.0%; Score 15.8; DB 4; Length 119032;
Best Local Similarity 78.9%; Pred. No. 3.6e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCU 19
    |||||:||||:|:|:|:
Db 60077 AACGGAGACAGGATGCCT 60059

RESULT 45
US-09-949-016-17268/c
; Sequence 17268, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17268
; LENGTH: 119032
; TYPE: DNA
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; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(119032)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17268

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 4; Length 119032;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGCTGGGAGCCU 19
DB 60077 AACGGAGCAGGGATGCC 60059

RESULT 46
US-09-949-016-13135/c
; Sequence 13135, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13135
; LENGTH: 7731
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13135

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 4; Length 7731;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGGCGGGAUGCCUU 20
DB 877 GGAGCGTGGATGCC 861

RESULT 47
US-09-902-540-1261
; Sequence 1261, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barty S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1261
; LENGTH: 34662
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1261

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 4; Length 34662;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 76.5%; Pred. No. 5.1e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGGCGGGAUGCCUU 20
DB 29422 GGAGGCGGATGCC 29438

RESULT 48
US-09-949-016-12797
; Sequence 12797, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12797
; LENGTH: 35262
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12797

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 4; Length 35262;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGGCGGGAUGCCUU 20
DB 22837 GGAGCGTGGATGCC 22853

RESULT 49
US-09-949-016-16399
; Sequence 16399, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16399
; LENGTH: 35263
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16399

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 4; Length 35263;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGGCGGGAUGCCUU 20
DB 22837 GGAGCGTGGATGCC 22853
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Db 22837 GGAGGCTGGGATGACTT 22853

RESULT 50

US-09-949-016-17008
; Sequence 17008, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17008
; LENGTH: 42246
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17008

Query Match 77.0%; Score 15.4; DB 4; Length 42246;
Best Local Similarity 76.5%; Pred. No. 5.2e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGGCTGGGATGACTT 20

|||||:|||||:

Db 35825 GGAGGCTGGGATGCCGT 35841

Search completed: May 24, 2005, 07:28:15
Job time : 170 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 05:28:41 ; Search time 5623 Seconds
(without alignments)

21.812 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacggagcggggaugccu 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 306160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 750 summaries

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Published Applications NA:*

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- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	100.0	720	17	US-10-148-953A-6
4	20	100.0	720	17	US-10-148-953A-7
5	20	100.0	720	17	US-10-148-953A-8
6	20	100.0	720	17	US-10-148-953A-9
7	20	100.0	720	17	US-10-148-953A-10
8	20	100.0	720	17	US-10-297-321-1
9	20	100.0	720	17	US-10-770-668-17
10	20	100.0	931	18	US-10-714-310-18
11	20	100.0	931	18	US-10-714-310-35
Sequence 1952, Ap					
Sequence 20, Appl					
Sequence 6, Appl					
Sequence 7, Appl					
Sequence 8, Appl					
Sequence 9, Appl					
Sequence 10, Appl					
Sequence 1, Appl					
Sequence 17, Appl					
Sequence 18, Appl					
Sequence 35, Appl					

Sequence 1, Appl	15	1050	100.0	20	US-10-072-830-1
Sequence 4, Appl	8	5086	100.0	20	US-08-726-211-4
Sequence 7, Appl	10	5086	100.0	20	US-09-993-420A-7
Sequence 11, Appl	16	5086	100.0	20	US-10-141-618-11
Sequence 4, Appl	16	5086	100.0	20	US-10-387-961A-4
Sequence 45, Appl	18	5086	100.0	20	US-10-825-282-45
Sequence 187, App	15	6030	100.0	20	US-10-171-581-187
Sequence 117, App	15	6030	100.0	20	US-10-007-926A-117
Sequence 508, App	17	6030	100.0	20	US-10-172-118-508
Sequence 289, App	17	6030	100.0	20	US-10-388-360-289
Sequence 508, App	17	6030	100.0	20	US-10-342-887-508
Sequence 1015, App	17	6030	100.0	20	US-10-641-643-1015
Sequence 170, App	18	6030	100.0	20	US-10-283-975A-170
Sequence 2, Appl	19	6030	100.0	20	US-10-479-832A-2
Sequence 13703, A	14	6142	100.0	20	US-10-198-846-13703
Sequence 55, Appl	20	85.0	85.0	17	US-10-422-466-55
Sequence 432, App	17	379	84.0	16.8	US-10-641-643-432
Sequence 20895, A	16	863	84.0	16.8	US-10-029-386-20895
Sequence 333, App	17	1154	84.0	16.8	US-10-120-988-333
Sequence 283795, A	13	530	82.0	31	US-10-027-632-283795
Sequence 283795, A	17	530	82.0	32	US-10-027-632-283795
Sequence 5615, Ap	18	45268	80.0	16	US-10-741-601-5615
Sequence 17564, A	19	45268	80.0	16	US-10-741-600-17564
Sequence 237467, A	13	650	79.0	35	US-10-027-632-237467
Sequence 237467, A	13	650	79.0	36	US-10-027-632-237467
Sequence 20300, A	13	718	79.0	37	US-10-027-632-20300
Sequence 17, Appl	17	718	79.0	38	US-10-027-632-20300
Sequence 17, Appl	18	1332	79.0	39	US-09-932-812-17
Sequence 17, Appl	18	1332	79.0	40	US-10-761-593A-17
Sequence 17, Appl	18	1368	79.0	41	US-09-968-362-17
Sequence 17, Appl	18	1368	79.0	42	US-10-800-449-17
Sequence 231, App	18	1368	79.0	43	US-10-800-449-17
Sequence 231, App	15	1701	79.0	44	US-10-156-761-231
Sequence 120535, A	18	2187	79.0	45	US-10-425-115-120535
Sequence 2510, Ap	15	2214	79.0	46	US-10-156-761-2510
Sequence 27879, A	17	3621	79.0	47	US-10-282-122A-27879
Sequence 9854, Ap	10	6149	79.0	48	US-09-764-891-9854
Sequence 9855, Ap	10	8031	79.0	49	US-09-764-891-9855
Sequence 9856, Ap	10	8066	79.0	50	US-09-764-891-9856
Sequence 2005, Ap	18	12382	79.0	51	US-10-723-860-2005
Sequence 1300, App	13	30030	79.0	52	US-10-087-192-1300
Sequence 7, Appl	13	31898	79.0	53	US-10-087-192-760
Sequence 3, Appl	14	60153	79.0	54	US-10-222-334-7
Sequence 1, Appl	15	82615	79.0	55	US-10-214-737-3
Sequence 1, Appl	15	9025608	79.0	56	US-10-156-761-1
Sequence 1, Appl	15	9025608	79.0	57	US-10-156-761-1
Sequence 10498, A	18	242	77.0	58	US-10-437-963-10498
Sequence 3152, Ap	18	279	77.0	59	US-10-430-201-3152
Sequence 3153, Ap	18	279	77.0	60	US-10-430-201-3153
Sequence 776, App	17	303	77.0	61	US-10-062-674-776
Sequence 25176, A	16	559	77.0	62	US-10-029-386-25176
Sequence 212693, A	13	585	77.0	63	US-10-027-632-212693
Sequence 212693, A	17	585	77.0	64	US-10-027-632-212693
Sequence 132907, A	17	684	77.0	65	US-10-424-599-132907
Sequence 20721, A	13	697	77.0	66	US-10-027-632-20721
Sequence 20721, A	17	697	77.0	67	US-10-027-632-20721
Sequence 5, Appl	9	769	77.0	68	US-09-952-571-5
Sequence 126000, A	13	835	77.0	69	US-10-027-632-126000
Sequence 126001, A	13	835	77.0	70	US-10-027-632-126001
Sequence 126002, A	13	835	77.0	71	US-10-027-632-126002
Sequence 126000, A	17	835	77.0	72	US-10-027-632-126000
Sequence 126001, A	17	835	77.0	73	US-10-027-632-126001
Sequence 12572, A	18	906	77.0	74	US-10-437-963-12572
Sequence 64, Appl	18	1176	77.0	75	US-10-473-126-64
Sequence 10, Appl	18	1185	77.0	76	US-10-789-493-10
Sequence 743, App	17	1777	77.0	77	US-10-044-090-743
Sequence 713, App	17	1840	77.0	78	US-10-388-934-713
Sequence 827, App	17	1840	77.0	79	US-10-388-934-827
Sequence 1604, Ap	17	2532	77.0	80	US-10-104-04-1604
Sequence 114365, A	13	2974	77.0	81	US-10-027-632-114365
Sequence 114365, A	17	2974	77.0	82	US-10-027-632-114365
Sequence 1526, Ap	17	3284	77.0	83	US-10-240-425-1526
Sequence 1526, Ap	17	3284	77.0	84	US-10-240-425-1526

C 85	15.4	77.0	23704	19	US-10-461-862-48	Sequence 48, Appl	C 158	15.2	76.0	5713	15	US-10-128-714-6062	Sequence 6062, Ap
C 86	15.4	77.0	31231	13	US-10-087-192-880	Sequence 880, App	C 159	15.2	76.0	7713	15	US-10-128-714-62	Sequence 62, Appl
C 87	15.4	77.0	3186	10	US-09-373-658-38	Sequence 38, Appl	C 160	15.2	76.0	7713	15	US-10-128-714-5062	Sequence 5062, Ap
C 88	15.4	77.0	3186	11	US-09-989-687-38	Sequence 38, Appl	C 161	15.2	76.0	9395	10	US-09-828-498-1	Sequence 1, Appl
C 89	15.4	77.0	43411	18	US-10-450-826-76	Sequence 76, Appl	C 162	15.2	76.0	42794	19	US-10-741-600-17670	Sequence 17670, A
C 90	15.4	77.0	59838	13	US-10-087-192-1702	Sequence 1702, App	C 163	15.2	76.0	193853	13	US-10-087-192-1663	Sequence 1663, Ap
C 91	15.4	77.0	96595	11	US-09-997-722-262	Sequence 262, App	C 164	15.2	76.0	227931	17	US-10-085-117-274	Sequence 274, App
C 92	15.4	77.0	127767	18	US-10-367-094-176	Sequence 176, App	C 165	15.2	76.0	684707	17	US-10-398-221-9	Sequence 9, Appl
C 93	15.4	77.0	183238	17	US-10-235-192A-47	Sequence 47, Appl	C 166	15.2	76.0	715517	13	US-10-027-632-53712	Sequence 53712, A
C 94	15.4	77.0	233800	17	US-10-087-192-652	Sequence 652, App	C 167	15.2	76.0	715517	17	US-10-027-632-53712	Sequence 53712, A
C 95	15.4	77.0	241805	18	US-10-741-601-5621	Sequence 5621, App	C 168	15.2	76.0	2256646	18	US-10-470-565-1	Sequence 1, Appl
C 96	15.4	77.0	241805	18	US-10-741-600-17581	Sequence 17581, A	C 169	15.2	76.0	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
C 97	15.2	76.0	20	16	US-10-365-623-21	Sequence 21, Appl	C 170	15.2	76.0	3186778	13	US-10-027-632-174961	Sequence 174961, A
C 98	15.2	76.0	25	19	US-10-719-900-75269	Sequence 75269, A	C 171	15.2	76.0	3186778	17	US-10-027-632-174961	Sequence 174961, A
C 99	15.2	76.0	162	17	US-10-242-535A-50918	Sequence 50918, A	C 172	15.2	76.0	3309400	9	US-09-738-626-1	Sequence 738, Appl
C 100	15.2	76.0	162	17	US-10-085-783A-50918	Sequence 50918, A	C 173	15	75.0	60	10	US-09-908-975-10089	Sequence 975, A
C 101	15.2	76.0	237	16	US-10-029-386-15608	Sequence 15608, A	C 174	15	75.0	254	17	US-10-424-549A-57	Sequence 549, Appl
C 102	15.2	76.0	349	18	US-10-425-115-67761	Sequence 67761, A	C 175	15	75.0	305	14	US-10-016-349A-57	Sequence 57, Appl
C 103	15.2	76.0	357	10	US-09-918-995-18923	Sequence 18923, A	C 176	15	75.0	574	9	US-09-822-849A-119	Sequence 119, App
C 104	15.2	76.0	380	18	US-10-437-963-3488	Sequence 83488, A	C 177	15	75.0	651	13	US-10-027-632-278636	Sequence 278636, A
C 105	15.2	76.0	404	18	US-10-437-963-65001	Sequence 65001, A	C 178	15	75.0	651	17	US-10-027-632-278636	Sequence 278636, A
C 106	15.2	76.0	492	10	US-09-918-995-33305	Sequence 33305, A	C 179	15	75.0	1670	15	US-10-190-012-2	Sequence 2, Appl
C 107	15.2	76.0	500	16	US-10-029-386-1908	Sequence 1908, App	C 180	15	75.0	1670	19	US-10-589-576-2	Sequence 589, A
C 108	15.2	76.0	505	11	US-09-864-408A-1913	Sequence 1913, App	C 181	15	75.0	1683	18	US-10-425-115-78080	Sequence 78080, A
C 109	15.2	76.0	548	18	US-10-437-963-14241	Sequence 14241, A	C 182	15	75.0	2402	18	US-10-437-963-14897	Sequence 14897, A
C 110	15.2	76.0	557	9	US-09-864-761-7574	Sequence 7574, App	C 183	15	75.0	2696	14	US-10-739-930-3943	Sequence 3943, Ap
C 111	15.2	76.0	559	9	US-09-974-300-8221	Sequence 8221, App	C 184	15	75.0	5279	14	US-10-116-949-5	Sequence 5, Appl
C 112	15.2	76.0	636	16	US-10-169-223-13	Sequence 13, Appl	C 185	15	75.0	5303	18	US-10-723-860-1798	Sequence 1798, Ap
C 113	15.2	76.0	637	13	US-10-027-632-125050	Sequence 125050, A	C 186	15	75.0	5463	14	US-10-116-949-1	Sequence 1, Appl
C 114	15.2	76.0	637	17	US-10-027-632-125050	Sequence 125050, A	C 187	15	75.0	5463	19	US-10-482-029-113	Sequence 113, App
C 115	15.2	76.0	648	13	US-10-027-632-266325	Sequence 266325, A	C 188	15	75.0	5482	14	US-10-116-949-3	Sequence 3, Appl
C 116	15.2	76.0	648	13	US-10-027-632-266326	Sequence 266326, A	C 189	15	75.0	5482	19	US-10-902-531-19	Sequence 19, Appl
C 117	15.2	76.0	648	17	US-10-027-632-266325	Sequence 266325, A	C 190	15	75.0	5583	18	US-10-723-860-6157	Sequence 6157, Ap
C 118	15.2	76.0	648	17	US-10-027-632-266326	Sequence 266326, A	C 191	15	75.0	5583	18	US-10-723-860-6157	Sequence 173, App
C 119	15.2	76.0	702	10	US-09-959-987-9	Sequence 9, Appl	C 192	15	75.0	5733	18	US-10-417-375-173	Sequence 171, App
C 120	15.2	76.0	723	18	US-10-425-115-44465	Sequence 44465, A	C 193	15	75.0	30752	13	US-10-087-192-745	Sequence 745, App
C 121	15.2	76.0	740	18	US-10-767-701-24500	Sequence 24500, A	C 194	15	75.0	140152	18	US-10-684-422-66	Sequence 66, App
C 122	15.2	76.0	764	13	US-10-027-632-142994	Sequence 142994, A	C 195	15	75.0	161051	18	US-10-417-375-170	Sequence 170, App
C 123	15.2	76.0	764	17	US-10-027-632-142994	Sequence 142994, A	C 196	15	75.0	161051	18	US-10-723-860-1452	Sequence 1452, Ap
C 124	15.2	76.0	926	9	US-09-734-846-1	Sequence 1, Appl	C 197	15	75.0	166181	19	US-10-723-860-3281	Sequence 3281, Ap
C 125	15.2	76.0	926	9	US-09-734-847A-39	Sequence 39, Appl	C 198	14.8	74.0	25	19	US-10-719-900-350318	Sequence 350318, A
C 126	15.2	76.0	926	9	US-09-952-278-5	Sequence 39, Appl	C 199	14.8	74.0	25	10	US-09-568-362-5	Sequence 5, Appl
C 127	15.2	76.0	926	15	US-10-072-830-3	Sequence 3, Appl	C 200	14.8	74.0	29	10	US-09-968-362-6	Sequence 6, Appl
C 128	15.2	76.0	926	16	US-10-302-262-1	Sequence 1, Appl	C 201	14.8	74.0	29	10	US-09-932-812-5	Sequence 5, Appl
C 129	15.2	76.0	926	17	US-10-402-017-1	Sequence 1, Appl	C 202	14.8	74.0	29	18	US-09-932-812-6	Sequence 6, Appl
C 130	15.2	76.0	926	17	US-10-641-643-1430	Sequence 1430, App	C 203	14.8	74.0	29	18	US-10-761-593A-5	Sequence 5, Appl
C 131	15.2	76.0	926	18	US-10-717-597-87	Sequence 87, Appl	C 204	14.8	74.0	29	18	US-10-761-593-6	Sequence 6, Appl
C 132	15.2	76.0	926	18	US-10-776-827-106	Sequence 106, App	C 205	14.8	74.0	29	18	US-10-800-497-6	Sequence 6, Appl
C 133	15.2	76.0	926	18	US-10-825-282-47	Sequence 47, App	C 206	14.8	74.0	29	18	US-10-800-497-6	Sequence 6, Appl
C 134	15.2	76.0	926	19	US-10-479-832A-3	Sequence 3, Appl	C 207	14.8	74.0	29	18	US-10-800-449-5	Sequence 5, Appl
C 135	15.2	76.0	1032	17	US-10-369-493-45049	Sequence 45049, A	C 208	14.8	74.0	29	18	US-10-800-449-5	Sequence 5, Appl
C 136	15.2	76.0	1236	18	US-10-792-517-1	Sequence 1, Appl	C 209	14.8	74.0	105	18	US-10-840-478-73	Sequence 73, Appl
C 137	15.2	76.0	1455	17	US-10-282-122A-42228	Sequence 42228, A	C 210	14.8	74.0	105	19	US-10-840-325-58	Sequence 58, Appl
C 138	15.2	76.0	1455	18	US-10-792-517-7	Sequence 7, Appl	C 211	14.8	74.0	106	18	US-10-840-325-59	Sequence 59, Appl
C 139	15.2	76.0	1455	19	US-10-496-207-38	Sequence 38, Appl	C 212	14.8	74.0	106	19	US-10-840-325-59	Sequence 59, Appl
C 140	15.2	76.0	1461	13	US-10-156-761-4214	Sequence 4214, App	C 213	14.8	74.0	201	18	US-10-719-993-6438	Sequence 6438, App
C 141	15.2	76.0	1610	13	US-10-027-632-258325	Sequence 258325, A	C 214	14.8	74.0	201	18	US-10-719-993-6471	Sequence 6471, Ap
C 142	15.2	76.0	1610	17	US-10-027-632-258325	Sequence 258325, A	C 215	14.8	74.0	201	18	US-10-719-993-6498	Sequence 6498, Ap
C 143	15.2	76.0	1835	17	US-10-369-493-36496	Sequence 36496, A	C 216	14.8	74.0	201	18	US-10-719-993-8480	Sequence 8480, Ap
C 144	15.2	76.0	1944	17	US-10-369-493-26410	Sequence 26410, A	C 217	14.8	74.0	201	18	US-10-719-993-8481	Sequence 8481, Ap
C 145	15.2	76.0	2193	9	US-09-738-626-1354	Sequence 1354, App	C 218	14.8	74.0	201	18	US-10-719-993-8486	Sequence 8486, Ap
C 146	15.2	76.0	2312	18	US-10-343-903-47	Sequence 47, Appl	C 219	14.8	74.0	256	18	US-10-437-963-62274	Sequence 62274, A
C 147	15.2	76.0	2316	18	US-10-781-014-361	Sequence 361, App	C 220	14.8	74.0	271	10	US-09-104-750-18	Sequence 18, Appl
C 148	15.2	76.0	2391	18	US-10-425-115-22499	Sequence 22499, A	C 221	14.8	74.0	296	18	US-10-425-115-1804	Sequence 1804, Ap
C 149	15.2	76.0	2520	18	US-10-437-963-14242	Sequence 14242, A	C 222	14.8	74.0	300	17	US-10-242-535A-48774	Sequence 48774, A
C 150	15.2	76.0	2775	18	US-10-437-963-19428	Sequence 19428, A	C 223	14.8	74.0	300	17	US-10-242-535A-48774	Sequence 48774, A
C 151	15.2	76.0	3062	18	US-10-398-037-86	Sequence 86, Appl	C 224	14.8	74.0	312	17	US-10-085-783A-48774	Sequence 48774, A
C 152	15.2	76.0	4044	17	US-10-320-797-228	Sequence 228, App	C 225	14.8	74.0	312	18	US-10-425-115-31890	Sequence 31890, A
C 153	15.2	76.0	4926	17	US-10-172-118-351	Sequence 351, App	C 226	14.8	74.0	359	9	US-09-983-965-4641	Sequence 4641, Ap
C 154	15.2	76.0	4926	17	US-10-342-887-351	Sequence 351, App	C 227	14.8	74.0	362	18	US-10-425-115-37018	Sequence 37018, A
C 155	15.2	76.0	5511	15	US-10-128-714-2062	Sequence 2062, App	C 228	14.8	74.0	425	18	US-10-425-115-145089	Sequence 145089, A
C 156	15.2	76.0	5574	15	US-10-128-714-7062	Sequence 7062, App	C 229	14.8	74.0	429	10	US-09-918-995-13992	Sequence 13992, A
C 157	15.2	76.0	5713	15	US-10-128-714-1062	Sequence 1062, App	C 230	14.8	74.0	445	18	US-10-425-115-1613	Sequence 1613, Ap

231	14.8	74.0	471	13	US-10-027-632-266611	Sequence 266611, App	304	14.8	74.0	3115	13	US-10-194-163-849	Sequence 849, App
232	14.8	74.0	471	13	US-10-027-632-266611	Sequence 266611, App	c 305	14.8	74.0	3141	10	US-09-975-719-12	Sequence 12, App
c 233	14.8	74.0	474	16	US-10-029-386-226617	Sequence 226617, A	c 306	14.8	74.0	3405	9	US-09-925-298-141	Sequence 141, App
c 234	14.8	74.0	491	10	US-09-918-995-9816	Sequence 9816, App	c 307	14.8	74.0	3405	14	US-10-102-806-141	Sequence 141, App
c 235	14.8	74.0	589	16	US-10-029-386-8732	Sequence 8732, App	c 308	14.8	74.0	3506	10	US-09-104-750-24	Sequence 24, App
236	14.8	74.0	613	13	US-10-027-632-26871	Sequence 26871, A	c 309	14.8	74.0	3533	13	US-10-027-632-114667	Sequence 114667, App
237	14.8	74.0	613	17	US-10-027-632-26871	Sequence 26871, A	c 310	14.8	74.0	3533	17	US-10-027-632-114667	Sequence 114667, App
c 238	14.8	74.0	648	18	US-10-425-115-128629	Sequence 128629, A	c 311	14.8	74.0	4005	9	US-09-349-015-24	Sequence 24, App
c 239	14.8	74.0	652	13	US-10-723-860-3900	Sequence 3900, App	c 312	14.8	74.0	4005	15	US-10-219-664-20	Sequence 20, App
c 240	14.8	74.0	661	13	US-10-087-192-2012	Sequence 2012, App	c 313	14.8	74.0	6108	17	US-10-416-314-110	Sequence 110, App
241	14.8	74.0	664	13	US-10-027-632-16935	Sequence 16935, A	c 314	14.8	74.0	6356	18	US-10-723-860-7816	Sequence 7816, App
242	14.8	74.0	664	17	US-10-027-632-16935	Sequence 16935, A	c 315	14.8	74.0	6716	18	US-10-719-993-407	Sequence 407, App
243	14.8	74.0	687	13	US-10-027-632-23044	Sequence 23044, A	c 316	14.8	74.0	6719	15	US-10-171-581-340	Sequence 340, App
244	14.8	74.0	687	13	US-10-027-632-23044	Sequence 23044, A	c 317	14.8	74.0	6719	18	US-10-883-436-9	Sequence 9, App
245	14.8	74.0	687	17	US-10-027-632-23044	Sequence 23044, A	c 318	14.8	74.0	7025	13	US-10-087-192-959	Sequence 959, App
246	14.8	74.0	687	17	US-10-027-632-23045	Sequence 23045, A	c 319	14.8	74.0	7994	18	US-10-719-993-408	Sequence 408, App
247	14.8	74.0	693	13	US-10-027-632-162611	Sequence 162611, App	c 320	14.8	74.0	8041	18	US-10-723-860-7892	Sequence 7892, App
248	14.8	74.0	693	17	US-10-027-632-162611	Sequence 162611, App	c 321	14.8	74.0	8249	16	US-10-240-965-138	Sequence 138, App
249	14.8	74.0	710	13	US-10-027-632-87679	Sequence 87679, A	c 322	14.8	74.0	8299	18	US-10-719-993-406	Sequence 406, App
250	14.8	74.0	710	17	US-10-027-632-87679	Sequence 87679, A	c 323	14.8	74.0	10328	19	US-10-840-325-129	Sequence 129, App
c 251	14.8	74.0	753	18	US-10-437-963-64512	Sequence 64512, A	c 324	14.8	74.0	12989	9	US-09-764-847-1489	Sequence 1489, App
c 252	14.8	74.0	755	17	US-10-294-934-314	Sequence 314, App	c 325	14.8	74.0	12989	14	US-10-092-154-1489	Sequence 1489, App
c 253	14.8	74.0	765	18	US-10-483-512-94	Sequence 94, App	c 326	14.8	74.0	14040	10	US-09-764-891-5478	Sequence 5478, App
c 254	14.8	74.0	765	13	US-10-027-632-131791	Sequence 131791, App	c 327	14.8	74.0	14040	10	US-09-764-891-5478	Sequence 5478, App
c 255	14.8	74.0	766	13	US-10-027-632-131792	Sequence 131792, App	c 328	14.8	74.0	14040	15	US-10-205-428-1004	Sequence 1004, App
c 256	14.8	74.0	766	17	US-10-027-632-131791	Sequence 131791, App	c 329	14.8	74.0	19929	10	US-09-764-891-9967	Sequence 9967, App
c 257	14.8	74.0	766	17	US-10-027-632-131792	Sequence 131792, App	c 330	14.8	74.0	20907	10	US-09-764-891-9967	Sequence 9967, App
c 258	14.8	74.0	798	10	US-09-975-719-30	Sequence 30, App	c 331	14.8	74.0	22183	18	US-10-719-993-6796	Sequence 6796, App
c 259	14.8	74.0	810	13	US-10-027-632-173009	Sequence 173009, App	c 332	14.8	74.0	22478	11	US-09-997-722-184	Sequence 184, App
c 260	14.8	74.0	810	17	US-10-027-632-173009	Sequence 173009, App	c 333	14.8	74.0	23328	11	US-09-997-722-184	Sequence 184, App
261	14.8	74.0	857	13	US-10-027-632-141858	Sequence 141858, App	c 334	14.8	74.0	26920	18	US-10-719-993-6969	Sequence 6969, App
262	14.8	74.0	857	17	US-10-027-632-141858	Sequence 141858, App	c 335	14.8	74.0	27589	11	US-09-997-722-190	Sequence 190, App
c 263	14.8	74.0	868	13	US-10-027-632-171989	Sequence 171989, App	c 336	14.8	74.0	32050	13	US-10-087-192-793	Sequence 793, App
c 264	14.8	74.0	868	17	US-10-027-632-171989	Sequence 171989, App	c 337	14.8	74.0	32461	18	US-10-322-281-697	Sequence 697, App
c 265	14.8	74.0	918	18	US-10-482-793-22	Sequence 22, App	c 338	14.8	74.0	34683	18	US-10-322-281-149	Sequence 149, App
c 266	14.8	74.0	918	18	US-10-482-793-22	Sequence 22, App	c 339	14.8	74.0	37305	18	US-10-719-993-6767	Sequence 6767, App
c 267	14.8	74.0	991	17	US-10-294-934-315	Sequence 315, App	c 340	14.8	74.0	42235	10	US-09-975-719-1	Sequence 1, App
c 268	14.8	74.0	1077	19	US-10-840-478-62	Sequence 62, App	c 341	14.8	74.0	49744	9	US-09-927-091-4	Sequence 4, App
c 269	14.8	74.0	1077	19	US-10-840-478-62	Sequence 62, App	c 342	14.8	74.0	57130	9	US-09-835-081-3	Sequence 3, App
c 270	14.8	74.0	1083	9	US-09-738-626-235	Sequence 235, App	c 343	14.8	74.0	67384	13	US-10-087-192-1363	Sequence 1363, App
c 271	14.8	74.0	1089	11	US-09-997-722-117	Sequence 117, App	c 344	14.8	74.0	68495	18	US-10-322-281-750	Sequence 750, App
c 272	14.8	74.0	1095	13	US-10-027-632-10101	Sequence 10101, A	c 345	14.8	74.0	77941	13	US-10-087-192-709	Sequence 709, App
c 273	14.8	74.0	1095	17	US-10-027-632-10101	Sequence 10101, A	c 346	14.8	74.0	87749	13	US-10-087-192-1768	Sequence 1768, App
c 274	14.8	74.0	1160	18	US-10-437-963-64516	Sequence 64516, A	c 347	14.8	74.0	96499	13	US-10-087-192-2011	Sequence 2011, App
c 275	14.8	74.0	1218	15	US-10-156-761-4360	Sequence 4360, App	c 348	14.8	74.0	111084	18	US-10-723-860-1627	Sequence 1627, App
c 276	14.8	74.0	1329	17	US-10-627-476-507	Sequence 507, App	c 349	14.8	74.0	164702	19	US-10-484-577-658	Sequence 658, App
c 277	14.8	74.0	1347	9	US-09-738-626-3055	Sequence 3055, App	c 350	14.8	74.0	204621	13	US-10-087-192-958	Sequence 958, App
c 278	14.8	74.0	1389	18	US-10-425-115-28218	Sequence 28218, A	c 351	14.8	74.0	254087	13	US-10-087-192-223	Sequence 223, App
c 279	14.8	74.0	1395	18	US-10-739-930-4648	Sequence 4648, App	c 352	14.8	74.0	290367	18	US-10-719-993-6887	Sequence 6887, App
c 280	14.8	74.0	1404	17	US-10-282-122A-33381	Sequence 33381, A	c 353	14.8	74.0	304905	17	US-10-271-416-1	Sequence 1, App
c 281	14.8	74.0	1407	10	US-09-975-719-28	Sequence 28, App	c 354	14.8	74.0	318760	18	US-10-719-993-6765	Sequence 6765, App
c 282	14.8	74.0	1410	9	US-09-815-242-7990	Sequence 7990, App	c 355	14.8	74.0	561515	18	US-10-741-601-5682	Sequence 5682, App
c 283	14.8	74.0	1410	17	US-10-282-122A-30603	Sequence 30603, A	c 356	14.8	74.0	561515	19	US-10-741-601-17730	Sequence 17730, App
c 284	14.8	74.0	1413	11	US-09-997-722-116	Sequence 116, App	c 357	14.8	74.0	608916	19	US-10-461-862-1	Sequence 1, App
c 285	14.8	74.0	1419	18	US-10-437-963-39461	Sequence 39461, A	c 358	14.8	74.0	3186778	13	US-10-027-632-174961	Sequence 174961, App
c 286	14.8	74.0	1738	9	US-09-444-783-3	Sequence 3, App	c 359	14.8	74.0	3186778	17	US-10-027-632-174961	Sequence 174961, App
c 287	14.8	74.0	1738	14	US-10-185-991-3	Sequence 3, App	c 360	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 288	14.8	74.0	1738	15	US-10-238-129-3	Sequence 3, App	c 361	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 289	14.8	74.0	1738	15	US-10-238-667-3	Sequence 3, App	c 362	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 290	14.8	74.0	1738	15	US-10-305-720-1402	Sequence 1402, App	c 363	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 291	14.8	74.0	1786	15	US-10-225-567A-35	Sequence 35, App	c 364	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 292	14.8	74.0	1886	17	US-10-094-749-1483	Sequence 1483, App	c 365	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 293	14.8	74.0	1889	17	US-10-108-260A-1046	Sequence 1046, App	c 366	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 294	14.8	74.0	2104	17	US-10-152-319A-1511	Sequence 1511, App	c 367	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 295	14.8	74.0	2104	17	US-10-486-706-288	Sequence 288, App	c 368	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 296	14.8	74.0	2244	17	US-10-120-801-27	Sequence 27, App	c 369	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 297	14.8	74.0	2258	17	US-10-104-047-209	Sequence 209, App	c 370	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 298	14.8	74.0	2373	18	US-10-437-963-50716	Sequence 50716, A	c 371	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 299	14.8	74.0	2537	18	US-10-322-281-150	Sequence 150, App	c 372	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 300	14.8	74.0	3017	18	US-09-104-750-23	Sequence 23, App	c 373	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 301	14.8	74.0	3102	15	US-10-155-895-5	Sequence 5, App	c 374	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 302	14.8	74.0	3103	9	US-09-925-302-115	Sequence 115, App	c 375	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 303	14.8	74.0	3103	10	US-09-925-302-115	Sequence 115, App	c 376	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App

C 377	14.4	72.0	294	18	US-10-437-963-70283	Sequence 70283, A	450	14.4	72.0	693	17	US-10-027-632-260565	Sequence 260565, A
C 378	14.4	72.0	318	10	US-09-975-719-336	Sequence 336, App	451	14.4	72.0	716	18	US-10-357-930-15101	Sequence 15101, A
C 379	14.4	72.0	324	18	US-10-437-963-18263	Sequence 18263, A	452	14.4	72.0	727	9	US-09-823-245A-139	Sequence 139, App
C 380	14.4	72.0	327	17	US-10-398-221-215	Sequence 215, App	453	14.4	72.0	741	17	US-10-062-674-1823	Sequence 1823, App
C 381	14.4	72.0	337	18	US-10-674-124A-20045	Sequence 20045, A	C 454	14.4	72.0	746	14	US-10-196-332-1	Sequence 1, Appli
C 382	14.4	72.0	357	18	US-10-425-115-4652	Sequence 4652, App	C 455	14.4	72.0	750	18	US-10-425-115-110611	Sequence 110611, App
C 383	14.4	72.0	358	18	US-10-425-115-100726	Sequence 100726, A	C 456	14.4	72.0	764	13	US-10-027-632-9882	Sequence 9882, App
C 384	14.4	72.0	374	18	US-10-357-930-15352	Sequence 15352, A	C 457	14.4	72.0	764	13	US-10-027-632-9882	Sequence 9882, App
C 385	14.4	72.0	390	18	US-10-425-115-169940	Sequence 169940, A	C 458	14.4	72.0	764	13	US-10-027-632-9882	Sequence 9882, App
C 386	14.4	72.0	398	19	US-10-696-639-811	Sequence 811, App	C 459	14.4	72.0	764	13	US-10-027-632-9882	Sequence 9882, App
C 387	14.4	72.0	401	9	US-09-764-887-98	Sequence 98, App	C 460	14.4	72.0	764	13	US-10-027-632-9882	Sequence 9882, App
C 388	14.4	72.0	401	14	US-10-073-961-98	Sequence 98, App	C 461	14.4	72.0	764	13	US-10-027-632-9882	Sequence 9882, App
C 389	14.4	72.0	404	14	US-10-357-930-36172	Sequence 36172, A	C 462	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 390	14.4	72.0	452	17	US-10-424-599-103409	Sequence 103409, A	C 463	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 391	14.4	72.0	466	10	US-09-918-995-33685	Sequence 33685, A	C 464	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 392	14.4	72.0	469	13	US-10-027-632-238440	Sequence 238440, A	C 465	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 393	14.4	72.0	469	13	US-10-027-632-238440	Sequence 238440, A	C 466	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 394	14.4	72.0	469	17	US-10-027-632-238440	Sequence 238440, A	C 467	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 395	14.4	72.0	469	17	US-10-027-632-238440	Sequence 238440, A	C 468	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 396	14.4	72.0	473	13	US-10-027-632-238441	Sequence 238441, A	C 469	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 397	14.4	72.0	473	17	US-10-027-632-316856	Sequence 316856, A	C 470	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 398	14.4	72.0	478	18	US-10-357-930-23769	Sequence 23769, A	C 471	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 399	14.4	72.0	478	18	US-10-357-930-23950	Sequence 23950, A	C 472	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 400	14.4	72.0	478	18	US-10-357-930-23950	Sequence 23950, A	C 473	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 401	14.4	72.0	478	18	US-10-357-930-23950	Sequence 23950, A	C 474	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 402	14.4	72.0	480	13	US-10-027-632-37635	Sequence 37635, A	C 475	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 403	14.4	72.0	480	13	US-10-027-632-37635	Sequence 37635, A	C 476	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 404	14.4	72.0	480	17	US-10-027-632-37635	Sequence 37635, A	C 477	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 405	14.4	72.0	480	17	US-10-027-632-37635	Sequence 37635, A	C 478	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 406	14.4	72.0	507	13	US-10-027-632-36114	Sequence 36114, A	C 479	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 407	14.4	72.0	507	17	US-10-027-632-36114	Sequence 36114, A	C 480	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 408	14.4	72.0	513	10	US-09-975-719-338	Sequence 338, App	C 481	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 409	14.4	72.0	516	16	US-10-029-386-11832	Sequence 11832, A	C 482	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 410	14.4	72.0	516	13	US-10-027-632-193055	Sequence 193055, A	C 483	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 411	14.4	72.0	516	17	US-10-027-632-193055	Sequence 193055, A	C 484	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 412	14.4	72.0	522	18	US-10-772-988-9	Sequence 9, Appli	C 485	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 413	14.4	72.0	525	13	US-10-027-632-61496	Sequence 61496, A	C 486	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 414	14.4	72.0	525	13	US-10-027-632-62402	Sequence 62402, A	C 487	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 415	14.4	72.0	525	13	US-10-027-632-62402	Sequence 62402, A	C 488	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 416	14.4	72.0	525	17	US-10-027-632-61496	Sequence 61496, A	C 489	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 417	14.4	72.0	525	17	US-10-027-632-62402	Sequence 62402, A	C 490	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 418	14.4	72.0	525	17	US-10-027-632-62402	Sequence 62402, A	C 491	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 419	14.4	72.0	525	17	US-10-398-221-393	Sequence 393, App	C 492	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 420	14.4	72.0	528	9	US-09-728-444-850	Sequence 850, App	C 493	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 421	14.4	72.0	528	18	US-10-357-930-57592	Sequence 57592, A	C 494	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 422	14.4	72.0	547	18	US-10-357-930-50826	Sequence 50826, A	C 495	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 423	14.4	72.0	553	9	US-09-964-824A-77	Sequence 77, Appli	C 496	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 424	14.4	72.0	553	9	US-09-964-824A-77	Sequence 77, Appli	C 497	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 425	14.4	72.0	553	19	US-10-843-611A-5380	Sequence 490, App	C 498	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 426	14.4	72.0	553	19	US-10-843-611A-5380	Sequence 490, App	C 499	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 427	14.4	72.0	559	9	US-09-880-107-1165	Sequence 1165, App	C 500	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 428	14.4	72.0	559	17	US-10-240-425-127	Sequence 127, App	C 501	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 429	14.4	72.0	577	13	US-10-027-632-292701	Sequence 292701, A	C 502	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 430	14.4	72.0	577	13	US-10-027-632-292701	Sequence 292701, A	C 503	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 431	14.4	72.0	586	16	US-10-029-386-12447	Sequence 12447, A	C 504	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 432	14.4	72.0	586	18	US-10-357-930-35929	Sequence 35929, A	C 505	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 433	14.4	72.0	586	18	US-10-357-930-44993	Sequence 44993, A	C 506	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 434	14.4	72.0	586	18	US-10-357-930-45230	Sequence 45230, A	C 507	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 435	14.4	72.0	594	18	US-10-767-701-6154	Sequence 6154, App	C 508	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 436	14.4	72.0	607	9	US-09-864-761-18555	Sequence 18555, A	C 509	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 437	14.4	72.0	611	18	US-10-425-115-110601	Sequence 110601, A	C 510	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 438	14.4	72.0	622	18	US-10-653-047-5305	Sequence 5305, App	C 511	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 439	14.4	72.0	623	18	US-10-653-047-5305	Sequence 5305, App	C 512	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 440	14.4	72.0	632	18	US-10-357-930-5932	Sequence 5932, App	C 513	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 441	14.4	72.0	650	13	US-10-027-632-203648	Sequence 203648, A	C 514	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 442	14.4	72.0	650	17	US-10-027-632-203648	Sequence 203648, A	C 515	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 443	14.4	72.0	651	13	US-10-027-632-291502	Sequence 291502, A	C 516	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 444	14.4	72.0	651	17	US-10-027-632-291502	Sequence 291502, A	C 517	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 445	14.4	72.0	664	13	US-10-027-632-291502	Sequence 291502, A	C 518	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 446	14.4	72.0	664	13	US-10-027-632-291502	Sequence 291502, A	C 519	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 447	14.4	72.0	664	17	US-10-027-632-291502	Sequence 291502, A	C 520	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 448	14.4	72.0	664	17	US-10-027-632-291502	Sequence 291502, A	C 521	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App
C 449	14.4	72.0	693	13	US-10-027-632-260565	Sequence 260565, A	C 522	14.4	72.0	818	13	US-10-027-632-9884	Sequence 9884, App

523	14.4	72.0	5914	9	US-09-764-878-303	Sequence 303, App	596	14.2	71.0	479	10	US-09-918-995-20165	Sequence 20165, A
524	14.4	72.0	5914	14	US-10-079-854-303	Sequence 303, App	597	14.2	71.0	480	17	US-10-152-319A-81	Sequence 81, Appl
525	14.4	72.0	6108	17	US-10-416-314-110	Sequence 110, App	598	14.2	71.0	481	9	US-09-864-761-11198	Sequence 11198, A
526	14.4	72.0	6266	17	US-10-276-312-1	Sequence 1, Appl	599	14.2	71.0	493	9	US-09-864-761-11148	Sequence 1148, Ap
527	14.4	72.0	6356	18	US-10-723-860-7816	Sequence 7816, Ap	600	14.2	71.0	494	18	US-10-767-701-14232	Sequence 14232, A
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529	14.4	72.0	10394	19	US-10-764-503-15	Sequence 15, Appl	602	14.2	71.0	502	10	US-09-918-995-20130	Sequence 20130, A
530	14.4	72.0	20633	18	US-10-322-281-852	Sequence 852, App	603	14.2	71.0	513	10	US-09-918-995-16230	Sequence 16230, A
531	14.4	72.0	30145	19	US-10-741-600-17588	Sequence 17588, A	604	14.2	71.0	513	10	US-09-918-995-22281	Sequence 22281, A
532	14.4	72.0	34668	19	US-09-900-449A-3	Sequence 3, Appl	605	14.2	71.0	514	10	US-09-764-891-7280	Sequence 7280, Ap
533	14.4	72.0	34668	13	US-10-480-934-3	Sequence 3, Appl	606	14.2	71.0	514	10	US-09-764-891-7382	Sequence 7382, Ap
534	14.4	72.0	37265	19	US-10-087-192-49	Sequence 49, Appl	607	14.2	71.0	517	18	US-10-767-701-1759	Sequence 1759, Ap
535	14.4	72.0	40050	17	US-10-052-482-91	Sequence 91, Appl	608	14.2	71.0	522	9	US-09-912-599-3	Sequence 3, Appl
536	14.4	72.0	40558	18	US-10-629-318-37	Sequence 37, Appl	609	14.2	71.0	525	18	US-10-437-963-62411	Sequence 62411, A
537	14.4	72.0	51323	18	US-10-417-375-135	Sequence 135, App	610	14.2	71.0	528	9	US-09-920-300A-1240	Sequence 1240, Ap
538	14.4	72.0	55836	18	US-10-322-281-433	Sequence 433, App	611	14.2	71.0	528	13	US-10-033-528-1240	Sequence 1240, Ap
539	14.4	72.0	59914	14	US-10-741-601-5619	Sequence 5619, Ap	612	14.2	71.0	528	16	US-10-099-926-1240	Sequence 1240, Ap
540	14.4	72.0	95845	13	US-10-087-192-1537	Sequence 1537, Ap	613	14.2	71.0	531	13	US-10-027-632-268276	Sequence 268276, A
541	14.4	72.0	122336	18	US-10-322-281-362	Sequence 362, App	614	14.2	71.0	531	13	US-10-027-632-268277	Sequence 268277, A
542	14.4	72.0	134841	13	US-10-087-192-1987	Sequence 1987, Ap	615	14.2	71.0	531	17	US-10-027-632-268276	Sequence 268276, A
543	14.4	72.0	169567	18	US-10-719-993-6774	Sequence 6774, Ap	616	14.2	71.0	531	17	US-10-027-632-268277	Sequence 268277, A
544	14.4	72.0	247682	17	US-10-235-192A-28	Sequence 28, Appl	617	14.2	71.0	546	16	US-10-029-385-19302	Sequence 19302, A
545	14.4	72.0	299598	14	US-10-322-696-16	Sequence 16, Appl	618	14.2	71.0	548	9	US-09-764-847-311	Sequence 311, App
546	14.4	72.0	304905	17	US-10-271-416-1	Sequence 1, Appl	619	14.2	71.0	548	14	US-10-092-154-311	Sequence 311, App
547	14.4	72.0	405660	18	US-10-322-696-82	Sequence 82, Appl	620	14.2	71.0	550	17	US-10-242-535A-2496	Sequence 2496, Ap
548	14.4	72.0	518360	18	US-10-367-094-125	Sequence 125, App	621	14.2	71.0	550	17	US-10-085-788A-2496	Sequence 2496, Ap
549	14.4	72.0	1163020	17	US-10-398-221-10	Sequence 10, Appl	622	14.2	71.0	551	13	US-10-027-632-91713	Sequence 91713, A
550	14.2	71.0	25	19	US-10-719-900-277707	Sequence 277707, A	623	14.2	71.0	551	17	US-10-027-632-91713	Sequence 91713, A
551	14.2	71.0	125	9	US-09-864-761-30110	Sequence 30110, A	624	14.2	71.0	552	18	US-10-021-323-4412	Sequence 4412, Ap
552	14.2	71.0	180	18	US-10-437-963-83385	Sequence 83385, A	625	14.2	71.0	553	13	US-10-027-632-151532	Sequence 151532, A
553	14.2	71.0	185	18	US-10-425-115-173939	Sequence 173939, A	626	14.2	71.0	553	17	US-10-027-632-151532	Sequence 151532, A
554	14.2	71.0	186	10	US-09-373-658-65	Sequence 65, Appl	627	14.2	71.0	553	13	US-10-027-632-235875	Sequence 235875, A
555	14.2	71.0	186	11	US-09-989-687-65	Sequence 65, Appl	628	14.2	71.0	559	17	US-10-027-632-235875	Sequence 235875, A
556	14.2	71.0	201	18	US-10-719-993-33671	Sequence 33671, A	629	14.2	71.0	567	16	US-10-029-386-5292	Sequence 5292, Ap
557	14.2	71.0	201	18	US-10-719-993-40186	Sequence 40186, A	630	14.2	71.0	569	18	US-10-425-115-130502	Sequence 130502, A
558	14.2	71.0	201	19	US-10-741-600-44277	Sequence 44277, A	631	14.2	71.0	570	9	US-09-864-761-13571	Sequence 13571, A
559	14.2	71.0	201	19	US-10-741-600-48915	Sequence 48915, A	632	14.2	71.0	581	9	US-09-770-152-154	Sequence 154, App
560	14.2	71.0	201	19	US-10-741-600-48916	Sequence 48916, A	633	14.2	71.0	584	13	US-10-027-632-186903	Sequence 186903, A
561	14.2	71.0	201	19	US-10-741-600-63095	Sequence 63095, A	634	14.2	71.0	584	17	US-10-027-632-186903	Sequence 186903, A
562	14.2	71.0	213	17	US-10-242-535A-2854	Sequence 2854, Ap	635	14.2	71.0	589	16	US-10-029-386-8728	Sequence 8728, Ap
563	14.2	71.0	213	17	US-10-085-783A-2854	Sequence 2854, Ap	636	14.2	71.0	589	16	US-10-029-386-12188	Sequence 12188, A
564	14.2	71.0	228	18	US-10-425-115-156193	Sequence 156193, A	637	14.2	71.0	594	13	US-10-027-632-180180	Sequence 180180, A
565	14.2	71.0	230	10	US-09-918-995-31717	Sequence 31717, A	638	14.2	71.0	594	17	US-10-027-632-180180	Sequence 180180, A
566	14.2	71.0	242	17	US-10-424-599-55808	Sequence 55808, A	639	14.2	71.0	597	13	US-10-027-632-146834	Sequence 146834, A
567	14.2	71.0	251	10	US-09-930-213-366	Sequence 366, App	640	14.2	71.0	597	16	US-10-029-386-5546	Sequence 5546, Ap
568	14.2	71.0	251	18	US-10-425-115-22971	Sequence 22971, A	641	14.2	71.0	597	17	US-10-027-632-146834	Sequence 146834, A
569	14.2	71.0	260	18	US-10-425-115-123165	Sequence 123165, A	642	14.2	71.0	598	18	US-10-021-323-3414	Sequence 3414, Ap
570	14.2	71.0	282	9	US-09-923-876-1066	Sequence 1066, App	643	14.2	71.0	610	13	US-10-027-632-99769	Sequence 99769, A
571	14.2	71.0	282	10	US-09-923-876-1066	Sequence 1066, App	644	14.2	71.0	610	17	US-10-027-632-99769	Sequence 99769, A
572	14.2	71.0	270	9	US-09-864-761-32216	Sequence 32216, A	645	14.2	71.0	610	17	US-10-027-632-99769	Sequence 99769, A
573	14.2	71.0	271	18	US-10-425-115-64672	Sequence 64672, A	646	14.2	71.0	626	13	US-10-027-632-141754	Sequence 141754, A
574	14.2	71.0	276	9	US-09-864-761-17915	Sequence 17915, A	647	14.2	71.0	632	18	US-10-653-047-2561	Sequence 2561, Ap
575	14.2	71.0	278	17	US-10-062-674-1703	Sequence 1703, App	648	14.2	71.0	632	18	US-10-767-701-8890	Sequence 8890, Ap
576	14.2	71.0	288	9	US-09-998-598-2462	Sequence 2462, App	649	14.2	71.0	636	14	US-10-198-846-8768	Sequence 8768, Ap
577	14.2	71.0	289	18	US-10-702-075-380	Sequence 380, App	650	14.2	71.0	636	14	US-10-198-846-8768	Sequence 8768, Ap
578	14.2	71.0	322	9	US-09-960-352-6206	Sequence 6206, App	651	14.2	71.0	657	17	US-10-437-963-75559	Sequence 75559, A
579	14.2	71.0	360	18	US-10-425-115-122917	Sequence 122917, A	652	14.2	71.0	657	17	US-10-425-115-162628	Sequence 162628, A
580	14.2	71.0	360	18	US-09-918-995-18089	Sequence 18089, A	653	14.2	71.0	661	18	US-10-425-115-63700	Sequence 63700, A
581	14.2	71.0	368	17	US-10-062-674-995	Sequence 995, App	654	14.2	71.0	667	18	US-10-425-115-162641	Sequence 162641, A
582	14.2	71.0	388	18	US-10-425-115-106319	Sequence 106319, A	655	14.2	71.0	669	18	US-10-437-963-75559	Sequence 75559, A
583	14.2	71.0	388	18	US-10-425-115-111291	Sequence 111291, A	656	14.2	71.0	677	13	US-10-027-632-135457	Sequence 135457, A
584	14.2	71.0	393	16	US-10-029-386-25888	Sequence 25888, A	657	14.2	71.0	677	13	US-10-027-632-135457	Sequence 135457, A
585	14.2	71.0	395	9	US-09-983-965-4875	Sequence 4875, Ap	658	14.2	71.0	677	17	US-10-027-632-135457	Sequence 135457, A
586	14.2	71.0	400	8	US-08-781-986A-2959	Sequence 2959, App	659	14.2	71.0	677	17	US-10-027-632-135457	Sequence 135457, A
587	14.2	71.0	400	17	US-10-329-624-2959	Sequence 2959, App	660	14.2	71.0	678	13	US-10-027-632-233144	Sequence 233144, A
588	14.2	71.0	406	9	US-09-770-423-672	Sequence 672, App	661	14.2	71.0	678	17	US-10-027-632-233144	Sequence 233144, A
589	14.2	71.0	416	10	US-09-918-995-17447	Sequence 17447, A	662	14.2	71.0	690	18	US-10-739-930-2237	Sequence 2237, Ap
590	14.2	71.0	417	18	US-10-437-963-93522	Sequence 93522, A	663	14.2	71.0	690	18	US-10-363-345A-25325	Sequence 25325, A
591	14.2	71.0	423	17	US-10-276-774-463	Sequence 463, App	664	14.2	71.0	690	18	US-10-363-345A-25325	Sequence 25325, A
592	14.2	71.0	435	10	US-09-918-995-20331	Sequence 20331, A	665	14.2	71.0	690	19	US-10-363-483A-25326	Sequence 25326, A
593	14.2	71.0	463	9	US-09-864-761-15711	Sequence 15711, A	666	14.2	71.0	690	19	US-10-363-483A-25326	Sequence 25326, A
594	14.2	71.0	468	18	US-10-357-930-3632	Sequence 3632, App	667	14.2	71.0	696	14	US-10-363-345A-2443	Sequence 2443, Ap
595	14.2	71.0	478	19	US-10-696-639-1200	Sequence 1200, App	668	14.2	71.0	696	18	US-10-363-345A-2444	Sequence 2444, Ap


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Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGATGCCCTT 593
Db 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 3
US-10-148-953A-6
; Sequence 6, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; PRIOR FILING DATE: 2003-04-10
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-148-953A-6

Query Match 100.0%; Score 20; DB 17; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGATGCCCTT 593
Db 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 4
US-10-148-953A-7
; Sequence 7, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; PRIOR FILING DATE: 2003-04-10
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-7

Query Match 100.0%; Score 20; DB 17; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGATGCCCTT 593
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Db 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 5
US-10-148-953A-8
; Sequence 8, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-8

Query Match 100.0%; Score 20; DB 17; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGATGCCCTT 593
Db 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 6
US-10-148-953A-9
; Sequence 9, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-9

Query Match 100.0%; Score 20; DB 17; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGATGCCCTT 593
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Db      574 AACGAGGCTGGGATGCCTT 593

RESULT 7
US-10-148-953A-10
; Sequence 10, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEAKU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING SAME, AND COMPOSITIONS CONTAINING THEM
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-10

Query Match      100.0%; Score 20; DB 17; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGATGCCTT 593
Db      574 AACGAGGCTGGGATGCCTT 593

RESULT 8
US-10-297-321-1
; Sequence 1, Application US/10297321
; Publication No. US20040072342A1
; GENERAL INFORMATION:
; APPLICANT: Bothwell, Alfred L. M.
; APPLICANT: Pober, Jordan S.
; APPLICANT: Schechner, Jeffrey S.
; APPLICANT: Zheng, Lian
; TITLE OF INVENTION: Production and Use of Microvessels in a
; TITLE OF INVENTION: Fibronectin-containing Gel
; FILE REFERENCE: 44574-5074-WO
; CURRENT APPLICATION NUMBER: US/10/297,321
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: US 60/208,931
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 60/279,797
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant Bcl-2
; OTHER INFORMATION: gene, D3A4
; NAME/KEY: CDS
; LOCATION: (1)..(720)
US-10-297-321-1

Query Match      100.0%; Score 20; DB 17; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGATGCCTT 593
Db      574 AACGAGGCTGGGATGCCTT 593

RESULT 9
US-10-770-668-17
; Sequence 17, Application US/10770668
; Publication No. US20040191843A1
; GENERAL INFORMATION:
; APPLICANT: Wright, Susan C.
; APPLICANT: Larrick, James W.
; APPLICANT: Nock, Steffen R.
; APPLICANT: Wilson, David S.
; TITLE OF INVENTION: Cell-Killing Molecules and Methods of Use Thereof
; FILE REFERENCE: ABSALUS-08602
; CURRENT APPLICATION NUMBER: US/10/770,668
; CURRENT FILING DATE: 2004-02-02
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-668-17

Query Match      100.0%; Score 20; DB 18; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGATGCCTT 593
Db      574 AACGAGGCTGGGATGCCTT 593

RESULT 10
US-10-714-310-18
; Sequence 18, Application US/10714310
; Publication No. US20040152654A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Zhidong
; APPLICANT: Ruffner, Duane B.
; APPLICANT: Prakash, Ramesh
; APPLICANT: Koehn, Richard
; TITLE OF INVENTION: Inhibitory Oligonucleotides Targeted to Bcl-2
; FILE REFERENCE: 12475/50102
; CURRENT APPLICATION NUMBER: US/10/714,310
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/426,269
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-714-310-18

Query Match      100.0%; Score 20; DB 18; Length 931;
Best Local Similarity 80.0%; Pred. No. 5.9;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGATGCCTT 642
Db      623 AACGAGGCTGGGATGCCTT 642

RESULT 11
US-10-714-310-35
; Sequence 35, Application US/10714310
; Publication No. US20040152654A1
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; GENERAL INFORMATION:
; APPLICANT: Chen, Zhidong
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Prakash, Ramesh
; APPLICANT: Koehn, Richard
; TITLE OF INVENTION: Inhibitory Oligonucleotides Targeted to Bcl-2
; FILE REFERENCE: 12475/50102
; CURRENT APPLICATION NUMBER: US/10/714,310
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/426,269
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-714-310-35

Query Match      100.0%; Score 20; DB 18; Length 931;
Best Local Similarity 80.0%; Pred. No. 5.9;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCGUGGAGCCUU 20
Db      623 AACGAGGCTGGGATGCCTT 642

RESULT 12
US-10-072-830-1
; Sequence 1, Application US/10072830
; Publication No. US20030103945A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, DONG PENG
; APPLICANT: HUANG, XIZHONG
; APPLICANT: CHEN, GUANG
; APPLICANT: MANJI, HUSSEINI K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING AXON
; TITLE OF INVENTION: REGENERATION AND PREVENTING NEURONAL CELL DEGENERATION
; FILE REFERENCE: ERM-105.01
; CURRENT APPLICATION NUMBER: US/10/072,830
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,832
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/272,617
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/289,990
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)..(748)
US-10-072-830-1

Query Match      100.0%; Score 20; DB 15; Length 1050;
Best Local Similarity 80.0%; Pred. No. 5.9;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCGUGGAGCCUU 20
Db      605 AACGAGGCTGGGATGCCTT 624

RESULT 13
US-08-726-211-4
; Sequence 4, Application US/08726211
; Publication No. US20030012812A1
; GENERAL INFORMATION:
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; APPLICANT: Tormo, Mar
; APPLICANT: Tari, Ana M.
; APPLICANT: Lopez-Berestein, Gabriel
; TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY
; TITLE OF INVENTION: LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,211
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: UTXC:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5086 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1459..2175
US-08-726-211-4

Query Match      100.0%; Score 20; DB 8; Length 5086;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCGUGGAGCCUU 20
Db      2032 AACGAGGCTGGGATGCCTT 2051

RESULT 14
US-09-993-420A-7
; Sequence 7, Application US/09993420A
; Publication No. US20030064476A1
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 01997/201006
; CURRENT APPLICATION NUMBER: US/09/993,420A
; CURRENT FILING DATE: 5001-11-09
; PRIOR APPLICATION NUMBER: 09/234,186
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 5086
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1459)...(2178)
US-09-993-420A-7

Query Match      100.0%; Score 20; DB 10; Length 5086;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAUGCCUU 20
|||||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 15
US-10-141-618-11
; Sequence 11, Application US/10141618
; Publication No. US20030165887A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods For Determining the Prognosis
; FILE REFERENCE: P-LJ 5254
; CURRENT APPLICATION NUMBER: US/10/141,618
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,233
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/356,934
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/388,221
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 5086
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1459)...(2178)
US-10-141-618-11

Query Match      100.0%; Score 20; DB 16; Length 5086;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAUGCCUU 20
|||||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 16
US-10-387-961A-4
; Sequence 4, Application US/10387961A
; Publication No. US20030219474A1
; GENERAL INFORMATION:
; APPLICANT: TORMO, ANA
; APPLICANT: TARI, MAR
; TITLE OF INVENTION: INHIBITION OF BCL-2 PROTEIN EXPRESSION BY LIPOSOMAL
; FILE REFERENCE: ANTISENSE OLIGODEOXYNUCLEOTIDES
; CURRENT APPLICATION NUMBER: US/10/387,961A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 08/726,211
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5086
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1459)..(2175)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-387-961A-4

Query Match      100.0%; Score 20; DB 17; Length 5086;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAUGCCUU 20
|||||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 17
US-10-825-282-45
; Sequence 45, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; FILE REFERENCE: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 5086
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1459)..(2178)
US-10-825-282-45

Query Match      100.0%; Score 20; DB 18; Length 5086;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAUGCCUU 20
|||||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 18
US-10-171-581-187
; Sequence 187, Application US/10171581
; Publication No. US20030104426A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: Linsley, Peter
; APPLICANT: Mao Mao
; TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia
; FILE REFERENCE: 9301-157-999
; CURRENT APPLICATION NUMBER: US/10/171,581
```

; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,914
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 366
; SEQ ID NO 187
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: M14745
; DATABASE ENTRY DATE: 2001-06-18
US-10-171-581-187

Query Match 100.0%; Score 20; DB 15; Length 6030;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGGAUGCCUU 20
|||||:||||:||||:
Db 605 AACGGAGCGCTGGGATGCCTT 624

RESULT 19

US-10-007-926A-117
; Sequence 117, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 117
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: b-cell cll/lymphoma 2 (BCL2) gene.
US-10-007-926A-117

Query Match 100.0%; Score 20; DB 15; Length 6030;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGGAUGCCUU 20
|||||:||||:||||:
Db 605 AACGGAGCGCTGGGATGCCTT 624

RESULT 20

US-10-172-118-508
; Sequence 508, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients

; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 508
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_000633
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-508

Query Match 100.0%; Score 20; DB 17; Length 6030;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGGAUGCCUU 20
|||||:||||:||||:
Db 605 AACGGAGCGCTGGGATGCCTT 624

RESULT 21

US-10-388-360-289
; Sequence 289, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffre B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 289
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-289

Query Match 100.0%; Score 20; DB 17; Length 6030;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGGAUGCCUU 20
|||||:||||:||||:
Db 605 AACGGAGCGCTGGGATGCCTT 624

RESULT 22

US-10-342-887-508
; Sequence 508, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene

```

; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 508
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-508

Query Match      100.0%; Score 20; DB 17; Length 6030;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGCGCGGGAUGCCUU 20
      |||||:||||:||||:||||:
Db      605 AACGGAGCGTGGGATGCCTT 624

RESULT 23
US-10-641-643-1015
; Sequence 1015, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
;             Susan G. Stuart
;             Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
;             GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1015:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6030 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: gi79370
; SEQUENCE DESCRIPTION: SEQ ID NO: 1015 :

```

```

US-10-641-643-1015

Query Match      100.0%; Score 20; DB 17; Length 6030;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGCGCGGGAUGCCUU 20
      |||||:||||:||||:||||:
Db      605 AACGGAGCGTGGGATGCCTT 624

RESULT 24
US-10-283-975A-170
; Sequence 170, Application US/10283975A
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 PCT
; CURRENT APPLICATION NUMBER: US/10/283,975A
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/340,938
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/338,997
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340,081
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/341,012
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: HUMAN
US-10-283-975A-170

Query Match      100.0%; Score 20; DB 18; Length 6030;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGCGCGGGAUGCCUU 20
      |||||:||||:||||:||||:
Db      605 AACGGAGCGTGGGATGCCTT 624

RESULT 25
US-10-479-832A-2
; Sequence 2, Application US/10479832A
; Publication No. US2005006407A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson Research Pty Ltd
; TITLE OF INVENTION: bcl-2 DNazymes
; FILE REFERENCE: WJPI3107942
; CURRENT APPLICATION NUMBER: US/10/479,832A
; CURRENT FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-479-832A-2

Query Match      100.0%; Score 20; DB 19; Length 6030;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGCGCGGGAUGCCUU 20
      |||||:||||:||||:||||:
Db      605 AACGGAGCGTGGGATGCCTT 624

```


RESULT 26
US-10-198-846-13703
; Sequence 13703, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13703
; LENGTH: 6142
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 3, 4, 6139, 6140, 6141, 6142
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13703
Query Match 100.0%; Score 20; DB 14; Length 6142;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AACGAGGCGGCGGAGCCUU 20
Db 590 AACGAGGCGTGGGATGCCTT 709
RESULT 27
US-10-422-466-55/c
; Sequence 55, Application US/10422466
; Publication No. US20040006036A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Ji-Fan
; APPLICANT: Bowersox, Scott
; TITLE OF INVENTION: Silencing transcription by methylation
; FILE REFERENCE: 112029, 00005
; CURRENT APPLICATION NUMBER: US/10/422,466
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: 09/643,128
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 60/196,749
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/214,148
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (19)
; OTHER INFORMATION: m5C at base 19
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor
US-10-422-466-55
Query Match 85.0%; Score 17; DB 17; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.2e+02;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AACGAGGCGGCGGAGCC 17
Db 17 AACGAGGCGTGGGATGC 1
RESULT 28
US-10-641-643-432/c
; Sequence 432, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Sellhauer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 432:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 1668184
; LIBRARY: BMARNOT03
; SEQUENCE DESCRIPTION: SEQ ID NO: 432 :
US-10-641-643-432
Query Match 84.0%; Score 16.8; DB 17; Length 379;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Oy 1 AACGAGGCGGCGGAGCCUU 20
Db 326 AGCGAGGCTGGGAGGCCTT 307
RESULT 29
US-10-029-386-20895/c
; Sequence 20895, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

```
/ FILE REFERENCE: ABOMICA-X-2
/ CURRENT APPLICATION NUMBER: US/10/029,386
/ CURRENT FILING DATE: 2001-12-20
/ NUMBER OF SEQ ID NOS: 34288
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 20895
/ LENGTH: 863
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC008762.5
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.81
/ OTHER INFORMATION: SWISSPROT HIT: P16053, EVALUATE 3.00e-08
/ OTHER INFORMATION: EST HUMAN HIT: B1518513.1, EVALUATE 0.00e+00
/ OTHER INFORMATION: NT HIT: G14767924, EVALUATE 0.00e+00
US-10-029-386-20895
```

```
Query Match 84.0%; Score 16.8; DB 16; Length 863;
Best Local Similarity 75.0%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 3; Mismatches 2;
```

```
QY 1 AACGGAGGCGUGGAUGCCUU 20
Db 264 AGCGAGGCTGGGAGGCCIT 245
|||||:|||||:|::
```

```
RESULT 30
US-10-120-988-333/c
/ Sequence 333, Application US/10120988
/ Publication No. US20030219745A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: Polypeptides
/ FILE REFERENCE: 802CON
/ CURRENT APPLICATION NUMBER: US/10/120,988
/ CURRENT FILING DATE: 2002-04-11
/ PRIOR APPLICATION NUMBER: 09/774,528
/ PRIOR FILING DATE: 2001-01-30
/ NUMBER OF SEQ ID NOS: 441
/ SOFTWARE: pt_FL_genes Version 2.0
/ SEQ ID NO 333
/ LENGTH: 1154
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1068)
US-10-120-988-333
```

```
Query Match 84.0%; Score 16.8; DB 17; Length 1154;
Best Local Similarity 70.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 AACGGAGGCGUGGAUGCCUU 20
Db 130 AAAGGAGTCTGGGATGCCIT 111
|||||:|||||:|::
```

```
RESULT 31
US-10-027-632-283795
/ Sequence 283795, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
```

```
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 283795
/ LENGTH: 530
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-283795
```

```
Query Match 82.0%; Score 16.4; DB 13; Length 530;
Best Local Similarity 72.2%; Pred. No. 3.2e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 CGGAGGCGUGGAUGCCUU 20
Db 140 CTGAGGCTGGGATGCCIT 157
|||||:|||||:|::
```

```
RESULT 32
US-10-027-632-283795
/ Sequence 283795, Application US/10027632
/ Publication No. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 283795
/ LENGTH: 530
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-283795
```

```
Query Match 82.0%; Score 16.4; DB 17; Length 530;
Best Local Similarity 72.2%; Pred. No. 3.2e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3  CGGAGGCGGGAUGCCUU 20
Db      140 CTGAGGCTGGGATGCCTT 157

RESULT 33
US-10-741-601-5615
; Sequence 5615, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5615
; LENGTH: 45268
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)...(45268)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-601-5615

Query Match      80.0%; Score 16; DB 18; Length 45268;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      5  GAGGCGGGAUGCCUU 20
Db      41704 GAGGCTGGATGCCTT 41719

RESULT 34
US-10-741-600-17564
; Sequence 17564, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17564
; LENGTH: 45268
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)...(45268)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17564

Query Match      80.0%; Score 16; DB 19; Length 45268;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      5  GAGGCGGGAUGCCUU 20
Db      41704 GAGGCTGGATGCCTT 41719

RESULT 35
US-10-027-632-237467/c
; Sequence 237467, Application US/10027632
; Publication No. US20020198371A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237467
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-237467

Query Match      79.0%; Score 15.8; DB 13; Length 650;
Best Local Similarity 78.9%; Pred. No. 6e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1  AACGGAGGCGGGAUGCCU 19
Db      212 AGCGAGGCTGGGAGGCCT 194

RESULT 36
US-10-027-632-237467/c
; Sequence 237467, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237467
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-237467

Query Match      79.0%; Score 15.8; DB 17; Length 650;
Best Local Similarity 78.9%; Pred. No. 6e+02;
```

Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGCCU 19
| | | | | : | | | | : | | | :
Db 212 AGCGGAGCGTGGGAGCCT 194

RESULT 37

US-10-027-632-20300/c
; Sequence 20300, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20300
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-20300

Query Match 79.0%; Score 15.8; DB 13; Length 718;
Best Local Similarity 73.7%; Pred. No. 6e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGCCU 19
| | | | | : | | | | : | | | :
Db 671 AAAGGAGCGTGGGAGCCT 653

RESULT 38

US-10-027-632-20300/c
; Sequence 20300, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20300
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-20300

Query Match 79.0%; Score 15.8; DB 17; Length 718;
Best Local Similarity 73.7%; Pred. No. 6e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGCCU 19
| | | | | : | | | | : | | | :
Db 671 AAAGGAGCGTGGGAGCCT 653

RESULT 39

US-09-932-812-17/c
; Sequence 17, Application US/09932812
; Publication No. US20030082749A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuEPO-L-vFc gamma2 (Figure 2A)
US-09-932-812-17

Query Match 79.0%; Score 15.8; DB 10; Length 1332;
Best Local Similarity 73.7%; Pred. No. 5.7e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGCGCGGAGCCUU 20
| | | | | : | | | | : | | | :
Db 977 ATGGAGCGTGGGAGCCTT 959

RESULT 40

US-10-761-593A-17/c
; Sequence 17, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuEPO-L-vFc gamma2 (Figure 2A)
US-10-761-593A-17

Query Match 79.0%; Score 15.8; DB 18; Length 1332;
Best Local Similarity 73.7%; Pred. No. 5.7e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCGGGGAGCCUU 20
Db 977 ATGGAGGCTGGGAGGCCTT 999

RESULT 41
US-10-968-362-17/c
; Sequence 17, Application US/09968362
; Publication No. US20030082679A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vfc gamma2 (Figure 2A)
US-10-968-362-17

Query Match 79.0%; Score 15.8; DB 10; Length 1368;
Best Local Similarity 73.7%; Pred. No. 5.6e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCGGGGAGCCUU 20
Db 1013 ATGGAGGCTGGGAGGCCTT 995

RESULT 42
US-10-800-497-17/c
; Sequence 17, Application US/10800497
; Publication No. US20040259209A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor with
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,497
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vfc gamma2 (Figure 2A)
US-10-800-497-17

Query Match 79.0%; Score 15.8; DB 18; Length 1368;
Best Local Similarity 73.7%; Pred. No. 5.6e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCGGGGAGCCUU 20

Db 1013 ATGGAGGCTGGGAGGCCTT 995

RESULT 43

US-10-800-449-17/c
; Sequence 17, Application US/10800449
; Publication No. US20040265973A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,449
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vfc gamma2 (Figure 2A)
US-10-800-449-17

Query Match 79.0%; Score 15.8; DB 18; Length 1368;
Best Local Similarity 73.7%; Pred. No. 5.6e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCGGGGAGCCUU 20
Db 1013 ATGGAGGCTGGGAGGCCTT 995

RESULT 44

US-10-156-761-231
; Sequence 231, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 231
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1701)
US-10-156-761-231

Query Match 79.0%; Score 15.8; DB 15; Length 1701;
Best Local Similarity 68.4%; Pred. No. 5.5e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCGGGGAGCCUU 20

Db 857 ACGGGTCTGGGATGCCTT 875
||||| :|||:|:::
||||| :|||:|:::

RESULT 45
US-10-425-115-120535/c
; Sequence 120535, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(3322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 120535
; LENGTH: 2187
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(2187)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_41411C.1
US-10-425-115-120535

Query Match 79.0%; Score 15.8; DB 18; Length 2187;
Best Local Similarity 73.7%; Pred. No. 5.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGGCGGAGCCU 19
| | | | | : | | | | | : | | | | | : | | | | | :
Db 78 ATCGGAGGCTGGGATGCCT 60

RESULT 46
US-10-156-761-2510/c
; Sequence 2510, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2510
; LENGTH: 2214
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2214)
US-10-156-761-2510

Query Match 79.0%; Score 15.8; DB 15; Length 2214;
Best Local Similarity 78.9%; Pred. No. 5.4e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGCGGCGGAGCCUU 20
| | | | | : | | | | | : | | | | | : | | | | | :
Db 1637 ACGGAGCGGCGGATGCCT 1619
||||| :|||:|:::
||||| :|||:|:::

RESULT 47
US-10-282-122A-27879
; Sequence 27879, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Hagelbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1'
; SEQ ID NO 27879
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Mycobacterium leprae
US-10-282-122A-27879

Query Match 79.0%; Score 15.8; DB 17; Length 3621;
Best Local Similarity 73.7%; Pred. No. 5.2e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGGCGGAGCCU 19
| | | | | : | | | | | : | | | | | : | | | | | :
Db 2691 ACGGAGGCTGGGATGCAT 2709
||||| :|||:|:::
||||| :|||:|:::

RESULT 48
US-09-764-891-9854/c
; Sequence 9854, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006

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OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 04:27:13 ; Search time 3973 Seconds
(without alignments)
205.502 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacggagcgggaugccu 20

Scoring table: IDENTITY NUC

Gapop 10'0 , Gapext 1.0

Searched: 4554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 750 summaries

Database : Pending Patents NA Main:

- 1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US06_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US07_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US080_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
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- 11: /cgn2_6/ptodata/1/pna/US085_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US086_COMB.seq.*
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- 16: /cgn2_6/ptodata/1/pna/US090_COMB.seq.*
- 17: /cgn2_6/ptodata/1/pna/US091_COMB.seq.*
- 18: /cgn2_6/ptodata/1/pna/US092A_COMB.seq.*
- 19: /cgn2_6/ptodata/1/pna/US092B_COMB.seq.*
- 20: /cgn2_6/ptodata/1/pna/US093A_COMB.seq.*
- 21: /cgn2_6/ptodata/1/pna/US093B_COMB.seq.*
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279	15.8	79.0	445	31	US-09-684-016-194727	Sequence 194727, A	C 352	15.8	79.0	3147	82	US-60-138-103-7680	Sequence 7680, Ap
280	15.8	79.0	445	62	US-10-767-795-8345	Sequence 8345, Ap	C 353	15.8	79.0	3621	1	PCT-US02-09107B-27879	Sequence 27879, A
281	15.8	79.0	455	22	US-09-404-284-203	Sequence 203, App	C 354	15.8	79.0	3621	51	US-10-282-122A-27879	Sequence 27879, A
282	15.8	79.0	455	23	US-09-524-038-203	Sequence 203, App	C 355	15.8	79.0	3999	27	US-09-614-150-19540	Sequence 19540, A
283	15.8	79.0	455	46	US-10-011-154-203	Sequence 203, App	C 356	15.8	79.0	3999	27	US-09-614-150A-19540	Sequence 19540, A
284	15.8	79.0	477	26	US-09-577-410-1267	Sequence 1267, Ap	C 357	15.8	79.0	3999	85	US-60-167-217-19680	Sequence 19680, A
285	15.8	79.0	480	26	US-09-572-409-75471	Sequence 75471, A	C 358	15.8	79.0	3999	88	US-60-131-637-19559	Sequence 19559, A
286	15.8	79.0	481	30	US-09-677-417-1398	Sequence 1398, Ap	C 359	15.8	79.0	6026	83	US-60-145-134-153	Sequence 153, App
287	15.8	79.0	481	62	US-10-745-457-1398	Sequence 1398, Ap	C 360	15.8	79.0	6149	1	PCT-US01-01339-9854	Sequence 9854, Ap
288	15.8	79.0	484	21	US-09-396-087-630	Sequence 630, App	C 361	15.8	79.0	6149	34	US-09-764-891-9854	Sequence 9854, Ap
289	15.8	79.0	508	24	US-09-539-806B-39837	Sequence 39837, A	C 362	15.8	79.0	6149	42	US-09-950-083-8234	Sequence 8234, Ap
290	15.8	79.0	508	24	US-09-539-806B-39837	Sequence 39837, A	C 363	15.8	79.0	6149	42	US-09-950-083B-8234	Sequence 8234, Ap
291	15.8	79.0	508	30	US-09-668-683-11968	Sequence 11968, A	C 364	15.8	79.0	6149	48	US-10-105-299-10385	Sequence 10385, A
292	15.8	79.0	508	85	US-60-168-614-1370	Sequence 3370, Ap	C 365	15.8	79.0	6149	64	US-10-868-184-8234	Sequence 8234, Ap
293	15.8	79.0	509	14	US-08-803-609-4156	Sequence 4156, Ap	C 366	15.8	79.0	6149	64	US-10-868-184B-8234	Sequence 8234, Ap
294	15.8	79.0	509	39	US-09-912-292-33243	Sequence 33243, A	C 367	15.8	79.0	6149	64	US-10-868-184B-8234	Sequence 8234, Ap
295	15.8	79.0	513	26	US-09-565-309A-45965	Sequence 45965, A	C 368	15.8	79.0	6149	64	US-10-868-194B-8234	Sequence 8234, Ap
296	15.8	79.0	513	77	US-60-082-300-16945	Sequence 16945, A	C 369	15.8	79.0	6149	64	US-10-896-164-8234	Sequence 8234, Ap
297	15.8	79.0	514	26	US-09-565-309A-41493	Sequence 41493, A	C 370	15.8	79.0	6343	22	US-09-404-520-886	Sequence 886, App
298	15.8	79.0	534	23	US-09-513-996A-72004	Sequence 72004, A	C 371	15.8	79.0	6343	22	US-09-404-520B-886	Sequence 886, App
299	15.8	79.0	534	26	US-09-565-309A-60175	Sequence 60175, A	C 372	15.8	79.0	8031	1	PCT-US01-01339-9855	Sequence 9855, Ap
300	15.8	79.0	543	23	US-09-513-996A-78867	Sequence 78867, A	C 373	15.8	79.0	8031	34	US-09-764-891-9855	Sequence 9855, Ap
301	15.8	79.0	550	26	US-09-565-309A-41494	Sequence 41494, A	C 374	15.8	79.0	8031	42	US-09-950-083-8235	Sequence 8235, Ap
302	15.8	79.0	582	95	US-60-253-651-25345	Sequence 25345, A	C 375	15.8	79.0	8031	42	US-09-950-083B-8235	Sequence 8235, Ap
303	15.8	79.0	598	98	US-60-288-292-46725	Sequence 46725, A	C 376	15.8	79.0	8031	48	US-10-105-299-10386	Sequence 10386, A
304	15.8	79.0	599	95	US-60-252-833-27254	Sequence 27254, A	C 377	15.8	79.0	8031	64	US-10-868-184-8235	Sequence 8235, Ap
305	15.8	79.0	601	2	PCT-US04-35274-39752	Sequence 39752, A	C 378	15.8	79.0	8031	64	US-10-868-184A-8235	Sequence 8235, Ap
306	15.8	79.0	601	66	US-10-940-774-20682	Sequence 20682, A	C 379	15.8	79.0	8031	64	US-10-868-184B-8235	Sequence 8235, Ap
307	15.8	79.0	601	66	US-10-940-774-20683	Sequence 20683, A	C 380	15.8	79.0	8031	64	US-10-868-194B-8235	Sequence 8235, Ap
308	15.8	79.0	601	66	US-10-940-774-20684	Sequence 20684, A	C 381	15.8	79.0	8031	64	US-10-896-164-8235	Sequence 8235, Ap
309	15.8	79.0	601	66	US-10-940-774-20685	Sequence 20685, A	C 382	15.8	79.0	8066	1	PCT-US01-01339-9856	Sequence 9856, Ap
310	15.8	79.0	601	66	US-10-940-774-128302	Sequence 128302, A	C 383	15.8	79.0	8066	34	US-09-764-891-9856	Sequence 9856, Ap
311	15.8	79.0	601	66	US-10-940-774-194506	Sequence 194506, A	C 384	15.8	79.0	12382	2	PCT-US03-38193-2005	Sequence 2005, Ap
312	15.8	79.0	601	66	US-10-940-774-194507	Sequence 194507, A	C 385	15.8	79.0	12382	62	US-10-723-860-2005	Sequence 2005, Ap
313	15.8	79.0	601	66	US-10-940-774-194507	Sequence 194507, A	C 386	15.8	79.0	12382	62	US-10-723-860-2005	Sequence 17413, A
314	15.8	79.0	601	66	US-10-940-774-202189	Sequence 202189, A	C 387	15.8	79.0	15511	66	US-10-940-774-17413	Sequence 11891, A
315	15.8	79.0	601	66	US-10-940-774-202190	Sequence 202190, A	C 388	15.8	79.0	15511	66	US-10-940-774-11891	Sequence 53338, A
316	15.8	79.0	601	66	US-10-940-774-202191	Sequence 202191, A	C 389	15.8	79.0	17082	116	US-60-465-241-53338	Sequence 87475, A
317	15.8	79.0	601	66	US-10-940-774-202192	Sequence 202192, A	C 390	15.8	79.0	17082	116	US-60-466-412-8475	Sequence 87475, A
318	15.8	79.0	650	28	US-09-634-306B-237467	Sequence 237467, A	C 391	15.8	79.0	17082	118	US-60-487-610-19959	Sequence 19959, A
319	15.8	79.0	700	87	US-60-182-316-10803	Sequence 10803, A	C 392	15.8	79.0	17082	128	US-60-582-609-19959	Sequence 19959, A
320	15.8	79.0	718	28	US-09-634-306B-20300	Sequence 20300, A	C 393	15.8	79.0	18963	34	US-09-760-475-4072	Sequence 96429, A
321	15.8	79.0	718	46	US-10-027-632-20300	Sequence 20300, A	C 394	15.8	79.0	20038	117	US-60-470-166-8993	Sequence 8993, Ap
322	15.8	79.0	803	102	US-60-324-185-33507	Sequence 33507, A	C 395	15.8	79.0	21292	42	US-09-950-083-5318	Sequence 5318, Ap
323	15.8	79.0	834	48	US-10-144-771-15759	Sequence 15759, A	C 396	15.8	79.0	21292	42	US-09-950-083B-5318	Sequence 5318, Ap
324	15.8	79.0	834	106	US-60-360-207-17579	Sequence 17579, A	C 397	15.8	79.0	21292	48	US-10-105-299-7469	Sequence 7469, Ap
325	15.8	79.0	877	22	US-09-471-275-9518	Sequence 9518, Ap	C 398	15.8	79.0	21292	64	US-10-868-184-5318	Sequence 5318, Ap
326	15.8	79.0	877	22	US-09-488-725B-981	Sequence 981, App	C 399	15.8	79.0	21292	64	US-10-868-184A-5318	Sequence 5318, Ap
327	15.8	79.0	877	26	US-09-552-317-981	Sequence 981, App	C 400	15.8	79.0	21292	64	US-10-868-184B-5318	Sequence 5318, Ap
328	15.8	79.0	888	22	US-09-404-520-19343	Sequence 19343, A	C 401	15.8	79.0	21292	64	US-10-868-184B-5318	Sequence 5318, Ap
329	15.8	79.0	888	22	US-09-404-520B-19343	Sequence 19343, A	C 402	15.8	79.0	21292	64	US-10-868-184B-5318	Sequence 5318, Ap
330	15.8	79.0	1332	40	US-09-932-812-17	Sequence 17, Appl	C 403	15.8	79.0	21910	86	US-60-172-360-27748	Sequence 5318, Ap
331	15.8	79.0	1332	40	US-09-932-812A-17	Sequence 17, Appl	C 404	15.8	79.0	22668	116	US-60-466-412-87473	Sequence 93692, A
332	15.8	79.0	1332	62	US-10-761-593A-17	Sequence 17, Appl	C 405	15.8	79.0	22668	67	US-10-990-328-93692	Sequence 84262, A
333	15.8	79.0	1332	68	US-11-017-185-17	Sequence 17, Appl	C 406	15.8	79.0	22668	66	US-10-940-774-13153	Sequence 13153, A
334	15.8	79.0	1368	63	US-10-800-449-17	Sequence 17, Appl	C 407	15.8	79.0	22668	92	US-60-230-445-849	Sequence 849, App
335	15.8	79.0	1368	63	US-10-800-449-17	Sequence 17, Appl	C 408	15.8	79.0	22668	92	US-60-230-445-849	Sequence 849, App
336	15.8	79.0	1512	48	US-10-144-771-875	Sequence 875, App	C 409	15.8	79.0	22668	116	US-60-466-412-84262	Sequence 84262, A
337	15.8	79.0	1512	106	US-60-360-207-875	Sequence 875, App	C 410	15.8	79.0	30030	47	US-10-087-192-1300	Sequence 1300, Ap
338	15.8	79.0	1701	49	US-10-156-761-231	Sequence 231, App	C 411	15.8	79.0	30519	83	US-60-144-351-1717	Sequence 1717, Ap
339	15.8	79.0	1914	22	US-09-417-507-17570	Sequence 17570, A	C 412	15.8	79.0	31898	47	US-10-087-192-760	Sequence 760, App
340	15.8	79.0	1944	27	US-09-614-150-19541	Sequence 19541, A	C 413	15.8	79.0	32768	90	US-60-212-655-73	Sequence 73, Appl
341	15.8	79.0	1944	27	US-09-614-150A-19541	Sequence 19541, A	C 414	15.8	79.0	32768	91	US-60-229-518-15	Sequence 15, Appl
342	15.8	79.0	1944	85	US-60-167-217-19681	Sequence 19681, A	C 415	15.8	79.0	32768	92	US-60-234-446-203	Sequence 203, App

416	15.8	79.0	33323	116	US-60-466-412-85341	Sequence 85341, A	489	15.4	77.0	201	116	US-60-466-412-40658	Sequence 40658, A
417	15.8	79.0	33370	28	US-09-620-392-7208	Sequence 7208, Ap	490	15.4	77.0	201	116	US-60-466-412-40659	Sequence 40659, A
418	15.8	79.0	35832	116	US-60-465-241-51650	Sequence 51650, A	C 491	15.4	77.0	201	116	US-60-466-412-207293	Sequence 207293, A
419	15.8	79.0	35832	118	US-60-487-610-19404	Sequence 19404, A	C 492	15.4	77.0	201	116	US-60-466-412-207294	Sequence 207294, A
420	15.8	79.0	35832	128	US-60-582-609-19404	Sequence 19404, A	C 493	15.4	77.0	201	116	US-60-466-412-211560	Sequence 211560, A
C 421	15.8	79.0	40592	65	US-10-932-349-19001	Sequence 19001, A	C 494	15.4	77.0	201	116	US-60-466-412-211561	Sequence 211561, A
C 422	15.8	79.0	40592	120	US-60-500-337-19001	Sequence 19001, A	C 495	15.4	77.0	201	116	US-60-466-412-210764	Sequence 210764, A
C 423	15.8	79.0	48120	32	US-09-702-134-5060	Sequence 5060, Ap	C 496	15.4	77.0	201	116	US-60-466-412-303707	Sequence 303707, A
C 424	15.8	79.0	48120	35	US-09-815-264-63365	Sequence 63365, A	C 497	15.4	77.0	201	116	US-60-466-412-303707	Sequence 303707, A
C 425	15.8	79.0	60075	65	US-10-932-333-11738	Sequence 11738, A	C 498	15.4	77.0	201	119	US-60-495-114-55864	Sequence 55864, A
C 426	15.8	79.0	60075	120	US-60-500-315-11738	Sequence 11738, A	C 499	15.4	77.0	229	16	US-09-016-866-529	Sequence 529, App
C 427	15.8	79.0	60153	1	PCT-US02-26285-7	Sequence 7, Appli	C 500	15.4	77.0	229	24	US-09-539-331D-18919	Sequence 18919, A
C 428	15.8	79.0	60153	50	US-10-222-334-7	Sequence 7, Appli	C 501	15.4	77.0	229	72	US-60-035-830-529	Sequence 529, App
C 429	15.8	79.0	65586	32	US-09-702-134-7410	Sequence 7410, Ap	C 502	15.4	77.0	242	36	US-09-837-604A-71300	Sequence 71300, A
C 430	15.8	79.0	65586	35	US-09-815-264-58505	Sequence 58505, A	C 503	15.4	77.0	242	36	US-09-837-604B-71300	Sequence 71300, A
C 431	15.8	79.0	65621	28	US-09-620-392-11024	Sequence 11024, A	C 504	15.4	77.0	242	54	US-10-437-963-10498	Sequence 10498, A
C 432	15.8	79.0	82615	33	US-09-739-014-3	Sequence 3, Appli	C 505	15.4	77.0	248	88	US-60-197-872-71170	Sequence 71170, A
C 433	15.8	79.0	82615	50	US-10-214-737-3	Sequence 3, Appli	C 506	15.4	77.0	248	15	US-08-984-691-2094	Sequence 2094, Ap
C 434	15.8	79.0	83516	66	US-10-940-774-15378	Sequence 15378, A	C 507	15.4	77.0	262	24	US-09-539-331D-30616	Sequence 30616, A
C 435	15.8	79.0	83838	32	US-09-702-134-4358	Sequence 4358, Ap	C 508	15.4	77.0	262	8	US-08-276-163A-13229	Sequence 13229, A
C 436	15.8	79.0	83838	35	US-09-815-264-79282	Sequence 79282, A	C 509	15.4	77.0	262	8	US-08-276-163B-13229	Sequence 13229, A
C 437	15.8	79.0	84846	67	US-10-990-328-93265	Sequence 93265, A	C 510	15.4	77.0	262	35	US-09-821-710-9265	Sequence 9265, Ap
C 438	15.8	79.0	87180	24	US-09-534-859-875	Sequence 875, App	C 511	15.4	77.0	262	36	US-09-840-145-13229	Sequence 13229, A
C 439	15.8	79.0	87180	35	US-09-803-736-875	Sequence 875, App	C 512	15.4	77.0	262	39	US-09-912-293-202258	Sequence 202258, A
C 440	15.8	79.0	94300	2	PCT-US04-23933-6	Sequence 6, Appli	C 513	15.4	77.0	279	2	PCT-US03-14114-3152	Sequence 3152, Ap
C 441	15.8	79.0	98690	1	PCT-US01-26663-1	Sequence 1, Appli	C 514	15.4	77.0	279	2	PCT-US03-14114-3152	Sequence 3152, Ap
C 442	15.8	79.0	119032	66	US-10-940-774-12160	Sequence 12160, A	C 515	15.4	77.0	279	54	US-10-430-201-3152	Sequence 3152, Ap
C 443	15.8	79.0	119032	66	US-10-940-774-17268	Sequence 17268, A	C 516	15.4	77.0	279	54	US-10-430-201-3153	Sequence 3153, Ap
C 444	15.8	79.0	125023	116	US-60-465-241-52687	Sequence 52687, A	C 517	15.4	77.0	303	28	US-09-625-102-776	Sequence 776, App
C 445	15.8	79.0	125023	116	US-60-466-412-85524	Sequence 85524, A	C 518	15.4	77.0	303	47	US-10-062-674-776	Sequence 776, App
C 446	15.8	79.0	125628	67	US-10-990-328-95531	Sequence 95531, A	C 519	15.4	77.0	341	33	US-09-515-128-15669	Sequence 15669, A
C 447	15.8	79.0	147237	67	US-10-990-328-94139	Sequence 94139, A	C 520	15.4	77.0	341	33	US-09-721-544-15669	Sequence 15669, A
C 448	15.8	79.0	154075	41	US-09-949-004-662	Sequence 662, App	C 521	15.4	77.0	400	21	US-09-362-510-56905	Sequence 56905, A
C 449	15.8	79.0	154075	41	US-09-949-004-663	Sequence 663, App	C 522	15.4	77.0	400	21	US-09-362-510A-56905	Sequence 56905, A
C 450	15.8	79.0	154075	68	US-11-009-711-662	Sequence 662, App	C 523	15.4	77.0	400	39	US-09-804-013-56905	Sequence 56905, A
C 451	15.8	79.0	154075	68	US-11-009-711-663	Sequence 663, App	C 524	15.4	77.0	412	37	US-09-866-555-9639	Sequence 9639, Ap
C 452	15.8	79.0	154125	95	US-60-258-250-59	Sequence 59, Appl	C 525	15.4	77.0	435	23	US-09-528-409-98064	Sequence 98064, A
C 453	15.8	79.0	158268	65	US-10-918-754-16901	Sequence 16901, A	C 526	15.4	77.0	435	40	US-09-933-524-98064	Sequence 98064, A
C 454	15.8	79.0	158268	119	US-60-495-114-16901	Sequence 16901, A	C 527	15.4	77.0	435	40	US-09-933-524A-98064	Sequence 98064, A
C 455	15.8	79.0	162075	116	US-60-465-241-53247	Sequence 53247, A	C 528	15.4	77.0	444	18	US-09-205-070-7194	Sequence 7194, Ap
C 456	15.8	79.0	162075	116	US-60-466-412-87342	Sequence 87342, A	C 529	15.4	77.0	444	18	US-09-340-623-7194	Sequence 7194, Ap
C 457	15.8	79.0	162346	65	US-10-932-333-11806	Sequence 11806, A	C 530	15.4	77.0	444	38	US-09-898-888-7194	Sequence 7194, Ap
C 458	15.8	79.0	162346	120	US-60-500-315-11806	Sequence 11806, A	C 531	15.4	77.0	444	38	US-09-898-888A-7194	Sequence 7194, Ap
C 459	15.8	79.0	201763	116	US-60-466-412-85509	Sequence 85509, A	C 532	15.4	77.0	477	20	US-09-306-350A-4541	Sequence 4541, Ap
C 460	15.8	79.0	367544	23	US-09-528-237A-886	Sequence 886, App	C 533	15.4	77.0	477	39	US-09-909-629-4541	Sequence 4541, Ap
C 461	15.8	79.0	604723	41	US-09-947-916-240	Sequence 240, App	C 534	15.4	77.0	480	21	US-09-362-510-59436	Sequence 59436, A
C 462	15.8	79.0	9025608	49	US-10-156-761-1	Sequence 1, Appli	C 535	15.4	77.0	480	21	US-09-362-510A-59436	Sequence 59436, A
C 463	15.8	79.0	9025608	49	US-10-156-761-1	Sequence 1, Appli	C 536	15.4	77.0	480	39	US-09-904-013-59436	Sequence 59436, A
C 464	15.4	77.0	25	43	US-09-956-584A-322162	Sequence 322162, A	C 537	15.4	77.0	487	49	US-10-170-235-43	Sequence 43, Appli
C 465	15.4	77.0	51	86	US-60-172-360-11586	Sequence 11586, A	C 538	15.4	77.0	487	115	US-60-452-680-5261	Sequence 5261, Ap
C 466	15.4	77.0	137	2	PCT-US03-26220-17162	Sequence 17162, A	C 539	15.4	77.0	487	115	US-60-453-050-3009	Sequence 3009, Ap
C 467	15.4	77.0	196	35	US-09-804-730-9763	Sequence 9763, Ap	C 540	15.4	77.0	487	115	US-60-453-135-3009	Sequence 3009, Ap
C 468	15.4	77.0	196	87	US-60-189-657-10012	Sequence 10012, A	C 541	15.4	77.0	487	116	US-60-466-412-3009	Sequence 3009, Ap
C 469	15.4	77.0	201	65	US-10-918-754-55864	Sequence 55864, A	C 542	15.4	77.0	517	95	US-60-253-651-12079	Sequence 12079, A
C 470	15.4	77.0	201	67	US-10-990-328-202031	Sequence 202031, A	C 543	15.4	77.0	523	33	US-09-758-474-401	Sequence 401, App
C 471	15.4	77.0	201	67	US-10-990-328-214862	Sequence 214862, A	C 544	15.4	77.0	523	50	US-10-213-068-401	Sequence 401, App
C 472	15.4	77.0	201	67	US-10-990-328-355604	Sequence 355604, A	C 545	15.4	77.0	523	50	US-10-213-068-401	Sequence 401, App
C 473	15.4	77.0	201	67	US-10-990-328-507450	Sequence 507450, A	C 546	15.4	77.0	524	49	US-10-170-235-124	Sequence 124, App
C 474	15.4	77.0	201	67	US-10-990-328-507451	Sequence 507451, A	C 547	15.4	77.0	524	115	US-60-452-680-5616	Sequence 5616, Ap
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ALIGNMENTS

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RESULT 1
US-10-018-437-2
; Sequence 2, Application US/10018437
; GENERAL INFORMATION:
; APPLICANT: ZANGEMEISTER-WITKE et al
; TITLE OF INVENTION: Oligonucleotide derivatives directed against human
; FILE REFERENCE: bcl-xL and human bcl-2 mRNA
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: US/10/018,437
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: PCT/EP00/03708
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(20)
; OTHER INFORMATION: Nucleotide nos. 2032 (5') to 2051 (3') of the
; OTHER INFORMATION: human bcl-2 mRNA; GenBank Accession No. M13994

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; PUBLICATION INFORMATION:
US-10-018-437-2
Query Match 100.0%; Score 20; DB 46; Length 20;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGAGGCGUGGAGCCUU 20
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Db 1 AACGAGGCGUGGAGCCUU 20
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RESULT 2
US-10-018-437-3/c
; Sequence 3, Application US/10018437
; GENERAL INFORMATION:
; APPLICANT: ZANGEMEISTER-WITKE et al
; TITLE OF INVENTION: Oligonucleotide derivatives directed against human
; FILE REFERENCE: bcl-xL and human bcl-2 mRNA
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: PCT/EP00/03708
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: GB 9910119.8
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Antisense
US-10-018-437-3
Query Match 100.0%; Score 20; DB 46; Length 20;
Best Local Similarity 80.0%; Pred. No. 67;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
US-09-660-080C-12703
; Sequence 12703, Application US/09660080C
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Toxicology
; FILE REFERENCE: 3109.1
; CURRENT APPLICATION NUMBER: US/09/660,080C
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/162,425
; PRIOR FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 20464
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 12703
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-660-080C-12703
Query Match 100.0%; Score 20; DB 30; Length 25;
Best Local Similarity 80.0%; Pred. No. 69;
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US-09-931-732C-31
; Sequence 31, Application US/09931732C
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES COMPRISING
; TITLE OF INVENTION: UNIVERSAL AND/OR DEGENERATE BASES
; FILE REFERENCE: OASBIO.001C1
; CURRENT APPLICATION NUMBER: US/09/931,732C
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/US00/09293
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/128,377
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primers
US-09-931-732C-31

Query Match      100.0%; Score 20; DB 40; Length 41;
Best Local Similarity 80.0%; Pred. No. 71;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
    |||||:||||:||||:
Db 13 AACGGAGGCTGGATGCCTT 32

RESULT 5
US-09-931-732D-31
; Sequence 31, Application US/09931732D
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES COMPRISING
; TITLE OF INVENTION: UNIVERSAL AND/OR DEGENERATE BASES
; FILE REFERENCE: GENP.001C1 (formerly OASBIO.001C1)
; CURRENT APPLICATION NUMBER: US/09/931,732D
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/US00/09293
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/128,377
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primers
US-09-931-732D-31

Query Match      100.0%; Score 20; DB 40; Length 41;
Best Local Similarity 80.0%; Pred. No. 71;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
    |||||:||||:||||:
Db 13 AACGGAGGCTGGATGCCTT 32

US-09-931-732C-31
; GENERAL INFORMATION:
; APPLICANT: Cuipepper, Janice A.
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2079-001
; CURRENT APPLICATION NUMBER: US/09/821,710
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/193,432
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 9938
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(368)
; OTHER INFORMATION: n = A,T,C or G
US-09-821-710-107

Query Match      100.0%; Score 20; DB 35; Length 368;
Best Local Similarity 80.0%; Pred. No. 83;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
    |||||:||||:||||:
Db 161 AACGGAGGCTGGATGCCTT 142

RESULT 7
US-09-760-476-1290
; Sequence 1290, Application US/09760476
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC015
; CURRENT APPLICATION NUMBER: US/09/760,476
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2602
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1290
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (395)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (403)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (410)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-760-476-1290

Query Match      100.0%; Score 20; DB 34; Length 432;
Best Local Similarity 80.0%; Pred. No. 84;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
    |||||:||||:||||:
Db 110 AACGGAGGCTGGATGCCTT 129

RESULT 8
US-09-760-485-82
; Sequence 82, Application US/09760485
; GENERAL INFORMATION:
```



```
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P217
; CURRENT APPLICATION NUMBER: US/09/760,485
; PRIOR FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1477
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (395)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (403)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (410)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-760-485-82
```

```
Query Match 100.0%; Score 20; DB 34; Length 432;
Best Local Similarity 80.0%; Pred. No. 84;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 AACGGAGGCGUGGAUGCUU 20
|||:||||:||||:||||:||||:
Db 110 AACGGAGGCTGGGATGCCT 129
```

```
RESULT 9
US-10-216-245-1290
; Sequence 1290, Application US/10216245
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P217
; CURRENT APPLICATION NUMBER: US/10/216,245
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/760,476
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2602
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1290
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (395)
; OTHER INFORMATION: n equals a,t,g, or c
```

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (403)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (410)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-216-245-1290
```

```
Query Match 100.0%; Score 20; DB 50; Length 432;
Best Local Similarity 80.0%; Pred. No. 84;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 AACGGAGGCGUGGAUGCUU 20
|||:||||:||||:||||:||||:
Db 110 AACGGAGGCTGGGATGCCT 129
```

```
RESULT 10
US-10-216-436-82
; Sequence 82, Application US/10216436
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P217C1N
; CURRENT APPLICATION NUMBER: US/10/216,436
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/760,485
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1477
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (395)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (403)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (410)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-216-436-82
```

```
Query Match 100.0%; Score 20; DB 50; Length 432;
Best Local Similarity 80.0%; Pred. No. 84;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 AACGGAGGCGGGAUGCCUU 20
|||||:||||:||||:
Db 110 AACGGAGGCTGGATGCCTT 129

RESULT 11
US-09-821-710-106/c
; Sequence 106, Application US/09821710
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice A.
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2079-001
; CURRENT APPLICATION NUMBER: US/09/821,710
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/193,432
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 9938
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(443)
; OTHER INFORMATION: n = A,T,C or G
US-09-821-710-106

Query Match 100.0%; Score 20; DB 35; Length 443;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
|||||:||||:||||:
Db 160 AACGGAGGCTGGATGCCTT 141

RESULT 12
US-09-528-409-40470
; Sequence 40470, Application US/09528409
; GENERAL INFORMATION:
; APPLICANT: Drmanac, Radoje T.
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Dickson, Mark
; APPLICANT: Jones, Lee W.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 774
; CURRENT APPLICATION NUMBER: US/09/528,409
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,453
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 116231
; SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 40470
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-528-409-40470

Query Match 100.0%; Score 20; DB 23; Length 454;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
|||||:||||:||||:
Db 104 AACGGAGGCTGGATGCCTT 123

RESULT 13
US-09-933-524-40470
; Sequence 40470, Application US/09933524
; GENERAL INFORMATION:
; APPLICANT: Drmanac, Radoje T.
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Dickson, Mark
; APPLICANT: Jones, Lee W.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 774
; CURRENT APPLICATION NUMBER: US/09/933,524
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 09/528,409
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 116231
; SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 40470
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-933-524-40470

Query Match 100.0%; Score 20; DB 40; Length 454;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
|||||:||||:||||:
Db 104 AACGGAGGCTGGATGCCTT 123

RESULT 14
US-09-933-524A-40470
; Sequence 40470, Application US/09933524A
; GENERAL INFORMATION:
; APPLICANT: Drmanac, Radoje T.
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Dickson, Mark
; APPLICANT: Jones, Lee W.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 774
; CURRENT APPLICATION NUMBER: US/09/933,524A
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 09/528,409
; PRIOR FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 116231
; SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 40470
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-933-524A-40470

Query Match 100.0%; Score 20; DB 40; Length 454;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
|||||:||||:||||:
Db 104 AACGGAGGCTGGATGCCTT 123

RESULT 15
PCT-US03-24625-3
; Sequence 3, Application PC/TUS0324625
; GENERAL INFORMATION:
; APPLICANT: Loma Linda University
; APPLICANT: ESCHER, Alan P.
; APPLICANT: Li, Fengchun

```

; TITLE OF INVENTION: Substances for Preventing and Treating Autoimmune Diseases
; FILE REFERENCE: 14102-1PCT
; CURRENT APPLICATION NUMBER: PCT/US03/24625
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: US 60/401,652
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-24625-3

Query Match      100.0%; Score 20; DB 2; Length 599;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAUGCCUU 20
   |||||:||||:||||:||||:
Db 439 AACGGAGGCTGGGATGCCTT 458

RESULT 16
PCT-US03-06196-36
; Sequence 36, Application PC/TUS0306196
; GENERAL INFORMATION:
; APPLICANT: PHASE-1 Molecular Toxicology, Inc.
; APPLICANT: Kier, Larry
; APPLICANT: Nolan, Timothy D.
; APPLICANT: Sankar, Usha
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Kidney Toxicity Predictive Genes
; FILE REFERENCE: 2874-020PCT
; CURRENT APPLICATION NUMBER: PCT/US03/06196
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 60/361,128
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: genes predictive for kidney tubular necrosis
; NAME/KEY: misc_feature
; LOCATION: 599, 612
; OTHER INFORMATION: n = A,T,C or G
PCT-US03-06196-36

Query Match      100.0%; Score 20; DB 2; Length 661;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAUGCCUU 20
   |||||:||||:||||:||||:
Db 494 AACGGAGGCTGGGATGCCTT 513

RESULT 17
PCT-US04-08371A-26
; Sequence 26, Application PC/TUS0408371A
; GENERAL INFORMATION:
; APPLICANT: Sankar, U.
; APPLICANT: Nolan, T.
; APPLICANT: Kier, I.
; APPLICANT: Derbel, M.
; TITLE OF INVENTION: Spleen Necrosis Predictive Genes
; FILE REFERENCE: 2874-021P
; CURRENT APPLICATION NUMBER: PCT/US04/08371A
; CURRENT FILING DATE: 2004-03-17
```

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; NUMBER OF SEQ ID NOS: 304
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Genes predictive for spleen necrosis
; NAME/KEY: misc_feature
; LOCATION: 599, 612
; OTHER INFORMATION: n = A,T,C or G
PCT-US04-08371A-26

Query Match      100.0%; Score 20; DB 2; Length 661;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAUGCCUU 20
   |||||:||||:||||:||||:
Db 494 AACGGAGGCTGGGATGCCTT 513

RESULT 18
US-10-060-893-433
; Sequence 433, Application US/10060893
; GENERAL INFORMATION:
; APPLICANT: Farris, Georgia
; APPLICANT: Hicken, Samuel H.
; APPLICANT: Farr, Spencer B.
; TITLE OF INVENTION: RAT TOXICOLOGICALLY RELEVANT GENES AND
; FILE REFERENCE: 400742000600
; CURRENT APPLICATION NUMBER: US/10/060,893
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/284,933
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/308,161
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 710
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 433
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 599, 612
; OTHER INFORMATION: n = A,T,C or G
US-10-060-893-433

Query Match      100.0%; Score 20; DB 47; Length 661;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAUGCCUU 20
   |||||:||||:||||:||||:
Db 494 AACGGAGGCTGGGATGCCTT 513

RESULT 19
US-10-298-226-433
; Sequence 433, Application US/10298226
; GENERAL INFORMATION:
; APPLICANT: Farr, Spencer B.
; APPLICANT: Farris, Georgia
; APPLICANT: Hicken, Samuel H.
; APPLICANT: Adkins, Karlessa
; APPLICANT: Neft, Robin E.
; APPLICANT: Pickett, Gavin
; TITLE OF INVENTION: RAT TOXICOLOGICALLY RELEVANT GENES AND
; FILE REFERENCE: 2874-003C
```

```
; CURRENT APPLICATION NUMBER: US/10/298,226
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 10/060,893
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 60/264,933
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/308,161
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 710
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 433
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 599..612
; OTHER INFORMATION: n = A,T,C or G
US-10-298-226-433

Query Match          100.0%; Score 20; DB 51; Length 661;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
Db 494 AACGGAGGCTGGGATGCCTT 513

RESULT 20
US-10-505-820-36
; Sequence 36, Application US/10505820
; GENERAL INFORMATION:
; APPLICANT: PHASE-1 Molecular Toxicology, Inc.
; APPLICANT: Kier, Larry
; APPLICANT: Nolan, Timothy D.
; APPLICANT: Sankar, Usha
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Kidney Toxicity Predictive Genes
; FILE REFERENCE: 2874-020PCT
; CURRENT APPLICATION NUMBER: US/10/505,820
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: PCT/US03/06196
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 60/361,128
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: genes predictive for kidney tubular necrosis
; NAME/KEY: misc feature
; LOCATION: 599..612
; OTHER INFORMATION: n = A,T,C or G
US-10-505-820-36

Query Match          100.0%; Score 20; DB 56; Length 661;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
Db 494 AACGGAGGCTGGGATGCCTT 513

RESULT 21
PCT-US04-17686-1766
; Sequence 1766, Application PC/TUS0417686
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
; APPLICANT: THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS
; TITLE OF INVENTION: PNI MICROARRAY AND USES
; FILE REFERENCE: 14114.0375PI
; CURRENT APPLICATION NUMBER: PCT/US04/17686
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/475,915
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 3085
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1766
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Mus musculus
PCT-US04-17686-1766

Query Match          100.0%; Score 20; DB 2; Length 711;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
Db 565 AACGGAGGCTGGGATGCCTT 584

RESULT 22
PCT-US04-17686-3015
; Sequence 3015, Application PC/TUS0417686
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
; APPLICANT: THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS
; TITLE OF INVENTION: PNI MICROARRAY AND USES
; FILE REFERENCE: 14114.0375PI
; CURRENT APPLICATION NUMBER: PCT/US04/17686
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/475,915
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 3085
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3015
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Mus musculus
PCT-US04-17686-3015

Query Match          100.0%; Score 20; DB 2; Length 711;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
Db 565 AACGGAGGCTGGGATGCCTT 584

RESULT 23
US-10-087-192-1952
; Sequence 1952, Application US/10087192
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

QY 1 AACGGAGGCGUGGAUGCCUU 20
Db 574 AACGGAGGCTGGGATGCCCT 593

RESULT 26
PCT-US94-10725-20
; Sequence 20, Application PC/TUS9410725
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10725
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brotman, Harris P.
; REGISTRATION NUMBER: 35461
; REFERENCE/DOCKET NUMBER: P0040W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-3630
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 717 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..717
PCT-US94-10725-20

Query Match 100.0%; Score 20; DB 1; Length 717;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
Db 574 AACGGAGGCTGGGATGCCCT 593

RESULT 27
US-08-124-256-20
; Sequence 20, Application US/08124256
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray, Cary, Ames & Frye
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/124,256
/ FILING DATE:
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Brotman, Harris F.
/ REGISTRATION NUMBER: 35461
/ REFERENCE/DOCKET NUMBER: P0041US0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 699-3630
/ TELEFAX: (619) 236-1048
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 717 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..717
/
US-08-124-256-20
```

```
Query Match 100.0%; Score 20; DB 7; Length 717;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AACGGAGGCGGGAUGCCUU 20
|||
Db 574 AACGGAGGCTGGGATGCCTT 593
```

RESULT 28

```
US-09-375-514A-20
/ Sequence 20, Application US/09375514A
/ GENERAL INFORMATION:
/ APPLICANT: Reed, John
/ TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
/ FILE REFERENCE: 10412-011
/ CURRENT APPLICATION NUMBER: US/09/375,514A
/ CURRENT FILING DATE: 1999-08-17
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 20
/ LENGTH: 717
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-375-514A-20
```

```
Query Match 100.0%; Score 20; DB 21; Length 717;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AACGGAGGCGGGAUGCCUU 20
|||
Db 574 AACGGAGGCTGGGATGCCTT 593
```

RESULT 29

```
US-09-375-514B-20
/ Sequence 20, Application US/09375514B
/ GENERAL INFORMATION:
/ APPLICANT: Reed, John
/ TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
/ FILE REFERENCE: 10412-011
/ CURRENT APPLICATION NUMBER: US/09/375,514B
/ CURRENT FILING DATE: 1999-08-17
/ PRIOR APPLICATION NUMBER: 09/080,285
/ PRIOR FILING DATE: 1998-05-16
/ PRIOR APPLICATION NUMBER: 08/465,485
/ PRIOR FILING DATE: 1995-06-25
```

```
/ PRIOR APPLICATION NUMBER: 08/124,256
/ PRIOR FILING DATE: 1993-09-20
/ PRIOR APPLICATION NUMBER: 07/840,716
/ PRIOR FILING DATE: 1992-02-21
/ PRIOR APPLICATION NUMBER: 07/288,692
/ PRIOR FILING DATE: 1998-12-22
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 20
/ LENGTH: 717
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-375-514B-20
```

```
Query Match 100.0%; Score 20; DB 21; Length 717;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AACGGAGGCGGGAUGCCUU 20
|||
Db 574 AACGGAGGCTGGGATGCCTT 593
```

RESULT 30

```
US-10-053-645A-20
/ Sequence 20, Application US/10053645A
/ GENERAL INFORMATION:
/ APPLICANT: Robert E. Klem
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
/ CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
/ FILE REFERENCE: 10412-022-999
/ CURRENT APPLICATION NUMBER: US/10/053,645A
/ CURRENT FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: 60/263,244
/ PRIOR FILING DATE: 2001-01-22
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 20
/ LENGTH: 717
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(717)
US-10-053-645A-20
```

```
Query Match 100.0%; Score 20; DB 47; Length 717;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AACGGAGGCGGGAUGCCUU 20
|||
Db 574 AACGGAGGCTGGGATGCCTT 593
```

RESULT 31

```
US-10-053-645B-20
/ Sequence 20, Application US/10053645B
/ GENERAL INFORMATION:
/ APPLICANT: Klem, Robert E.
/ TITLE OF INVENTION: Methods and Compositions for Treating a Cell-Proliferative
/ CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2 Antisense Oligomers,
/ FILE REFERENCE: 112475/51002
/ CURRENT APPLICATION NUMBER: US/10/053,645B
/ CURRENT FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: US 60/263,244
/ PRIOR FILING DATE: 2001-01-22
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 20
/ LENGTH: 717
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-053-645B-20

Query Match      100.0%; Score 20; DB 47; Length 717;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCGUGGGAUGCCUU 20
      |||||:||||:||||:||||:
Db      574 AACGGAGGCTGGGATGCCTT 593

RESULT 32
PCT-US01-18034-1
; Sequence 1, Application PC/TUS0118034
; GENERAL INFORMATION:
; APPLICANT: Bothwell, Alfred L. M.
; APPLICANT: Pober, Jordan S.
; APPLICANT: Schechner, Jeffrey S.
; APPLICANT: Zheng, Lian
; TITLE OF INVENTION: Production and Use of Microvessels in a
; FILE REFERENCE: Fibronectin-containing Gel
; CURRENT APPLICATION NUMBER: PCT/US01/18034
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/208,931
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 60/279,797
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant Bcl-2
; NAME/KEY: CDS
; LOCATION: (1)..(720)
PCT-US01-18034-1

Query Match      100.0%; Score 20; DB 1; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCGUGGGAUGCCUU 20
      |||||:||||:||||:||||:
Db      574 AACGGAGGCTGGGATGCCTT 593

RESULT 33
PCT-US03-11371-1
; Sequence 1, Application PC/TUS0311371
; GENERAL INFORMATION:
; APPLICANT: Bothwell, Alfred L. M.
; APPLICANT: Pober, Jordan S.
; APPLICANT: Schechner, Jeffrey S.
; APPLICANT: Yale University
; TITLE OF INVENTION: Vascularized Human Skin Equivalent
; FILE REFERENCE: 44574-5124-WO
; CURRENT APPLICATION NUMBER: PCT/US03/11371
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/371,677
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-053-645B-20

Query Match      100.0%; Score 20; DB 20; DB 2; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCGUGGGAUGCCUU 20
      |||||:||||:||||:||||:
Db      574 AACGGAGGCTGGGATGCCTT 593

RESULT 34
PCT-US04-02974-17
; Sequence 17, Application PC/TUS0402974
; GENERAL INFORMATION:
; APPLICANT: Wright, Susan C.
; APPLICANT: Larrick, James W.
; APPLICANT: Nock, Steffen R.
; APPLICANT: Wilson, David S.
; TITLE OF INVENTION: Cell-Killing Molecules and Methods of Use Thereof
; FILE REFERENCE: ABSALUS-08804
; CURRENT APPLICATION NUMBER: PCT/US04/02974
; CURRENT FILING DATE: 2004-02-02
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(720)
PCT-US04-02974-17

Query Match      100.0%; Score 20; DB 20; DB 2; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCGUGGGAUGCCUU 20
      |||||:||||:||||:||||:
Db      574 AACGGAGGCTGGGATGCCTT 593

RESULT 35
PCT-US04-17686-25
; Sequence 25, Application PC/TUS0417686
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
; APPLICANT: THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS
; APPLICANT: FOR DISEASE CONTROL AND PREVENTION
; TITLE OF INVENTION: PNI MICROARRAY AND USES
; FILE REFERENCE: 14114.0375P1
; CURRENT APPLICATION NUMBER: PCT/US04/17686
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/475,915
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 3085
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(720)
PCT-US04-17686-25

Query Match      100.0%; Score 20; DB 20; DB 2; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AACGGAGCGGCGGAGCCUU 20
    |||||:||||:||||:||||:
Db 574 AACGGAGCGTGGGATGCCTT 593

RESULT 36
PCT-US04-30849-3
; Sequence 3, Application PC/TUS0430849
; GENERAL INFORMATION:
; APPLICANT: Emory University
; APPLICANT: Feinberg, Mark
; APPLICANT: Garber, David
; TITLE OF INVENTION: IMPROVED MVA VACCINES
; FILE REFERENCE: 50508-2360
; CURRENT APPLICATION NUMBER: PCT/US04/30849
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/504,030
; PRIOR FILING DATE: 2003-09-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 720
; TYPE: DNA
; ORGANISM: homo sapiens
PCT-US04-30849-3

Query Match 100.0%; Score 20; DB 2; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGGCGGAGCCUU 20
    |||||:||||:||||:||||:
Db 574 AACGGAGCGTGGGATGCCTT 593

RESULT 37
US-10-148-953A-6
; Sequence 6, Application US/10148953A
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING SAME, AND COMPOSITIONS CONTAINING THEM
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-148-953A-6

Query Match 100.0%; Score 20; DB 48; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGGCGGAGCCUU 20
    |||||:||||:||||:||||:
Db 574 AACGGAGCGTGGGATGCCTT 593

RESULT 38
US-10-148-953A-7
; Sequence 7, Application US/10148953A
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING SAME, AND COMPOSITIONS CONTAINING THEM
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-7

Query Match 100.0%; Score 20; DB 48; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGGCGGAGCCUU 20
    |||||:||||:||||:||||:
Db 574 AACGGAGCGTGGGATGCCTT 593

RESULT 39
US-10-148-953A-8
; Sequence 8, Application US/10148953A
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING SAME, AND COMPOSITIONS CONTAINING THEM
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-8

Query Match 100.0%; Score 20; DB 48; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGGCGGAGCCUU 20
    |||||:||||:||||:||||:
Db 574 AACGGAGCGTGGGATGCCTT 593

RESULT 40
US-10-148-953A-9
; Sequence 9, Application US/10148953A
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING SAME, AND COMPOSITIONS CONTAINING THEM
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-9

Query Match 100.0%; Score 20; DB 48; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```



```
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-9

Query Match      100.0%; Score 20; DB 48; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCTGGGAUGCCUU 20
        |||||:||||:||||:||||:
Db      574 AACGGAGGCTGGGATGCTT 593

RESULT 41
US-10-148-953A-10
; Sequence 10, Application US/10148953A
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUNA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING SAME, AND COMPOSITIONS CONTAINING THEM
; FILE REFERENCE: 7389/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-10

Query Match      100.0%; Score 20; DB 48; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCTGGGAUGCCUU 20
        |||||:||||:||||:||||:
Db      574 AACGGAGGCTGGGATGCTT 593

RESULT 42
US-10-297-321-1
; Sequence 1, Application US/10297321
; GENERAL INFORMATION:
; APPLICANT: Bothwell, Alfred L. M.
; APPLICANT: Pober, Jordan S.
; APPLICANT: Schechner, Jeffrey S.
; APPLICANT: Zheng, Lian
; TITLE OF INVENTION: Production and Use of Microvessels in a
; TITLE OF INVENTION: Fibronectin-containing Gel
; FILE REFERENCE: 44574-5074-WO
; CURRENT APPLICATION NUMBER: US/10/297,321
```

```
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: US 60/208,931
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 60/279,797
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant Bcl-2
; OTHER INFORMATION: Gene, D34A
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(720)
US-10-297-321-1

Query Match      100.0%; Score 20; DB 51; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCTGGGAUGCCUU 20
        |||||:||||:||||:||||:
Db      574 AACGGAGGCTGGGATGCTT 593

RESULT 43
US-10-510-816-1
; Sequence 1, Application US/10510816
; GENERAL INFORMATION:
; APPLICANT: Bothwell, Alfred L. M.
; APPLICANT: Pober, Jordan S.
; APPLICANT: Schechner, Jeffrey S.
; APPLICANT: Yale University
; TITLE OF INVENTION: Vascularized Human Skin Equivalent
; FILE REFERENCE: 44574-5124-WO
; CURRENT APPLICATION NUMBER: US/10/510,816
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 60/371,677
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant Bcl-2
; OTHER INFORMATION: gene, D34A
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(720)
US-10-510-816-1

Query Match      100.0%; Score 20; DB 56; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCTGGGAUGCCUU 20
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Db      574 AACGGAGGCTGGGATGCTT 593

RESULT 44
US-10-770-668-17
; Sequence 17, Application US/10770668
; GENERAL INFORMATION:
; APPLICANT: Wright, Susan C.
; APPLICANT: Larrick, James W.
; APPLICANT: Nock, Steffen R.
; APPLICANT: Wilson, David S.
```

;
; TITLE OF INVENTION: Cell-Killing Molecules and Methods of Use Thereof
; FILE REFERENCE: ABSALUS-08602
; CURRENT APPLICATION NUMBER: US/10/770,668
; CURRENT FILING DATE: 2004-02-02
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-668-17

Query Match 100.0%; Score 20; DB 62; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGGCCUU 20
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DB 574 AACGGAGGCTGGGATGCCTT 593

RESULT 45
US-10-958-691-2
; Sequence 2, Application US/10958691
; GENERAL INFORMATION:
; APPLICANT: Harlan, John M.
; APPLICANT: Winn, Robert K.
; APPLICANT: Iwata, Akiko
; APPLICANT: Tupper, Joan
; APPLICANT: Li, John
; TITLE OF INVENTION: BCL-2 DERIVATIVES, AND METHODS OF USE
; FILE REFERENCE: UWOTL123265
; CURRENT APPLICATION NUMBER: US/10/958,691
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-958-691-2

Query Match 100.0%; Score 20; DB 66; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGGCCUU 20
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DB 574 AACGGAGGCTGGGATGCCTT 593

RESULT 46
US-60-371-677-1
; Sequence 1, Application US/60371677
; GENERAL INFORMATION:
; APPLICANT: Bothwell, Alfred L. M.
; APPLICANT: Pober, Jordan S.
; APPLICANT: Schechner, Jeffrey S.
; APPLICANT: Zheng, Lian
; TITLE OF INVENTION: Vascularized Human Skin Equivalent
; FILE REFERENCE: 44574-5074-P2
; CURRENT APPLICATION NUMBER: US/60/371,677
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/208,931
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 60/279,797
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

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; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant Bcl-2
; OTHER INFORMATION: gene, D34A
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(720)
US-60-371-677-1

Query Match 100.0%; Score 20; DB 107; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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DB 574 AACGGAGGCTGGGATGCCTT 593

RESULT 47
US-11-021-541-1706
; Sequence 1706, Application US/11021541
; GENERAL INFORMATION:
; APPLICANT: REICH, SAMUEL JOTHAM
; APPLICANT: TOLENTINO, MICHAEL J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE
; FILE REFERENCE: DER-04-1324R
; CURRENT APPLICATION NUMBER: US/11/021,541
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,099
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 1733
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1706
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(709)
US-11-021-541-1706

Query Match 100.0%; Score 20; DB 68; Length 741;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGGCCUU 20
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DB 566 AACGGAGGCTGGGATGCCTT 585

RESULT 48
US-08-403-721-1
; Sequence 1, Application US/08403721
; GENERAL INFORMATION:
; APPLICANT: EVAN, Gerald Ian
; TITLE OF INVENTION: Modified Cells And Methods Of Treatment
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,721

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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00686
; FILING DATE: 02 APRIL 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HENRY N. WIXON
; REFERENCE/DOCKET NUMBER: 104322.139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 942-8400
; TELEFAX: (202) 942-8484
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 765 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 18
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..747
; US-08-403-721-1

Query Match 100.0%; Score 20; DB 10; Length 765;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 604 AACGGAGGCTGGGATGCTT 623
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RESULT 49

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US-09-958-215-1
; Sequence 1, Application US/09958215
; GENERAL INFORMATION:
; APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
; TITLE OF INVENTION: Processes for screening apoptotic inhibitor or
; FILE REFERENCE: A081-01PCT
; CURRENT APPLICATION NUMBER: US/09/958,215
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: JP P1999-101888
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)..(751)
; OTHER INFORMATION: Human Bcl-2 protein
US-09-958-215-1
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Query Match 100.0%; Score 20; DB 43; Length 771;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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RESULT 50

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US-11-021-541-1704
; Sequence 1704, Application US/11021541
; GENERAL INFORMATION:
; APPLICANT: REICH, SAMUEL JOTHAM
; APPLICANT: TOLENTINO, MICHAEL J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE
; FILE REFERENCE: DBR-04-1324R
; CURRENT APPLICATION NUMBER: US/11/021,541
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,099
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 1733
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1704
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(775)
; US-11-021-541-1704

Query Match 100.0%; Score 20; DB 68; Length 777;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 602 AACGGAGGCTGGGATGCTT 621
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacgagggcgggaugccuu 20

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Searched: 12243922 seqs, 153826366 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 750 summaries

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SUMMARIES

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4	20	100.0	777	2	PCT-US04-43454-1704
5	20	100.0	5086	9	US-10-961-458-19
6	20	100.0	6030	9	US-10-887-066-1
7	20	100.0	6145	14	US-60-659-397-671
8	18.4	92.0	201	7	US-10-990-328A-203044
9	18.4	92.0	665590	7	US-10-990-328A-94275
10	18	90.0	21	10	US-10-941-663A-247
11	18	90.0	23	10	US-10-941-663A-248
12	17.4	87.0	2779	8	US-10-450-763-19742
13	17	85.0	21	10	US-10-941-663A-361
14	17	85.0	23	10	US-10-941-663A-362
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16	16.8	84.0	596	1	PCT-US04-43830-45
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18	16.8	84.0	3051	9	US-10-489-448-205
19	16.8	84.0	4206	11	US-11-097-143-38803

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Sequence 19546, A
Sequence 14030, A
Sequence 19540, A
Sequence 96429, A
Sequence 93692, A
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Sequence 95531, A
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Sequence 34295, A
Sequence 35719, A
Sequence 44440, A
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Sequence 3620, Ap
Sequence 2344, Ap
Sequence 18933, A
Sequence 6990, Ap
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Sequence 19, Appl
Sequence 14, Appl

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94	15.2	76.0	768	1	US-10-703-032-26665	Sequence 26665, A	c 167	14.8	74.0	565	9	US-10-703-032-21732	Sequence 21732, A
c 95	15.2	76.0	966	14	US-60-669-241-22797	Sequence 22797, A	c 168	14.8	74.0	581	1	PCT-US05-00517-2613	Sequence 2613, App
96	15.2	76.0	1252	1	PCT-US05-00517-3417	Sequence 3417, App	c 169	14.8	74.0	599	9	US-10-972-079-92756	Sequence 92756, A
c 97	15.2	76.0	1410	2	PCT-US05-00370-41	Sequence 41, Appl	c 170	14.8	74.0	600	12	US-11-060-756-227	Sequence 227, App
c 98	15.2	76.0	2250	12	US-11-079-463-1487	Sequence 1487, App	c 171	14.8	74.0	600	12	US-11-060-756-4499	Sequence 4499, App
c 99	15.2	76.0	2250	12	US-11-079-045-1487	Sequence 1487, App	c 172	14.8	74.0	606	14	US-60-655-875-93191	Sequence 93191, A
c 100	15.2	76.0	2373	12	US-11-079-463-1491	Sequence 1491, App	c 173	14.8	74.0	738	12	US-11-031-175-6309	Sequence 6309, App
101	15.2	76.0	2373	12	US-11-079-045-1491	Sequence 1491, App	c 174	14.8	74.0	889	14	US-60-669-241-12250	Sequence 12250, A
102	15.2	76.0	2575	1	PCT-US05-10257-713	Sequence 713, App	c 175	14.8	74.0	961	11	US-11-097-143-15980	Sequence 15980, A
103	15.2	76.0	3110	8	US-10-450-763-8503	Sequence 8503, App	c 176	14.8	74.0	965	9	US-10-703-032-31108	Sequence 31108, A
c 104	15.2	76.0	3591	11	US-11-097-143-41362	Sequence 41362, A	c 177	14.8	74.0	999	14	US-60-669-241-13954	Sequence 13954, A
105	15.2	76.0	4832	2	PCT-US04-05292A-28	Sequence 28, Appl	c 178	14.8	74.0	1077	12	US-11-024-545-53	Sequence 53, Appl
106	15.2	76.0	4832	2	PCT-US04-05292A-29	Sequence 29, Appl	c 179	14.8	74.0	1128	9	US-10-703-032-604	Sequence 604, App
107	15.2	76.0	4832	2	PCT-US04-05292A-28	Sequence 28, Appl	c 180	14.8	74.0	1194	12	US-11-055-822-733	Sequence 733, App
108	15.2	76.0	4832	2	PCT-US04-05292A-29	Sequence 29, Appl	c 181	14.8	74.0	1218	12	US-11-031-175-5628	Sequence 5628, App
109	15.2	76.0	6187	2	PCT-US04-05292A-16	Sequence 16, Appl	c 182	14.8	74.0	1498	12	US-11-031-175-385	Sequence 385, App
110	15.2	76.0	6187	2	PCT-US04-05292A-22	Sequence 22, Appl	c 183	14.8	74.0	1803	8	US-10-450-763-4191	Sequence 4191, A
111	15.2	76.0	6187	2	PCT-US04-05292A-16	Sequence 16, Appl	c 184	14.8	74.0	1961	7	US-10-990-328A-5017	Sequence 5017, App
112	15.2	76.0	6187	2	PCT-US04-05292A-22	Sequence 22, Appl	c 185	14.8	74.0	1961	11	US-11-085-606-1278	Sequence 1278, App
113	15.2	76.0	6452	2	PCT-US04-05292A-17	Sequence 17, Appl	c 186	14.8	74.0	2104	1	PCT-US05-11532-478	Sequence 478, App
114	15.2	76.0	6452	2	PCT-US04-05292A-23	Sequence 23, Appl	c 187	14.8	74.0	2104	1	PCT-US05-11532-479	Sequence 479, App
115	15.2	76.0	6452	2	PCT-US04-05292A-17	Sequence 17, Appl	c 188	14.8	74.0	2104	12	US-11-036-196-1511	Sequence 1511, App
116	15.2	76.0	7182	2	PCT-US04-05292A-23	Sequence 23, Appl	c 189	14.8	74.0	2247	8	US-10-450-763-18399	Sequence 18399, A
117	15.2	76.0	7182	14	US-60-659-397-793	Sequence 793, App	c 190	14.8	74.0	2579	11	US-11-097-143-36682	Sequence 36682, A
118	15.2	76.0	7390	7	US-10-990-328A-6955	Sequence 6955, App	c 191	14.8	74.0	2771	11	US-11-097-143-18812	Sequence 18812, A
119	15.2	76.0	7390	14	US-60-659-397-794	Sequence 794, App	c 192	14.8	74.0	3029	14	US-60-659-397-524	Sequence 524, App
120	15.2	76.0	11078	7	US-10-990-328A-2814	Sequence 2814, App	c 193	14.8	74.0	3030	7	US-10-990-328A-5021	Sequence 5021, App
121	15.2	76.0	11681	7	US-10-990-328A-2815	Sequence 2815, App	c 194	14.8	74.0	3030	11	US-11-085-606-1272	Sequence 1272, App
122	15.2	76.0	11681	7	US-10-990-328A-2818	Sequence 2818, App	c 195	14.8	74.0	3078	11	US-11-097-143-9793	Sequence 9793, App
123	15.2	76.0	11742	7	US-10-990-328A-2816	Sequence 2816, App	c 196	14.8	74.0	4140	11	US-11-097-143-3371	Sequence 3371, App
124	15.2	76.0	12347	2	PCT-US04-05292A-24	Sequence 24, Appl	c 197	14.8	74.0	4193	8	US-10-450-763-20870	Sequence 20870, A
125	15.2	76.0	12347	2	PCT-US04-05292A-26	Sequence 26, Appl	c 198	14.8	74.0	4845	11	US-11-097-143-28291	Sequence 28291, A
126	15.2	76.0	12347	2	PCT-US04-05292A-24	Sequence 24, Appl	c 199	14.8	74.0	5338	11	US-11-097-143-18811	Sequence 18811, A
127	15.2	76.0	12347	2	PCT-US04-05292A-26	Sequence 26, Appl	c 200	14.8	74.0	8165	12	US-11-024-545-64	Sequence 64, Appl
128	15.2	76.0	12612	2	PCT-US04-05292A-25	Sequence 25, Appl	c 201	14.8	74.0	8382	11	US-11-097-143-3370	Sequence 3370, App
129	15.2	76.0	12612	2	PCT-US04-05292A-25	Sequence 25, Appl	c 202	14.8	74.0	8748	11	US-11-097-143-15979	Sequence 15979, A
130	15.2	76.0	12612	2	PCT-US04-05292A-25	Sequence 25, Appl	c 203	14.8	74.0	12536	11	US-11-097-143-27781	Sequence 27781, A
131	15.2	76.0	12612	2	PCT-US04-05292A-27	Sequence 27, Appl	c 204	14.8	74.0	12690	12	US-11-024-545-52	Sequence 52, Appl
c 132	15.2	76.0	19499	7	US-10-990-328A-97351	Sequence 97351, A	c 205	14.8	74.0	12690	12	US-11-024-545-52	Sequence 52, Appl
133	15.2	76.0	27915	7	US-10-990-328A-94482	Sequence 94482, A	c 206	14.8	74.0	15328	7	US-10-990-328A-97426	Sequence 97426, A
c 134	15.2	76.0	34677	12	US-11-033-545-593	Sequence 593, App	c 207	14.8	74.0	15741	7	US-10-990-328A-96918	Sequence 96918, A
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136	15.2	76.0	54590	7	US-10-990-328A-95953	Sequence 95953, A	c 209	14.8	74.0	30429	7	US-10-990-328A-97657	Sequence 97657, A
137	15.2	76.0	55015	14	US-60-659-397-12250	Sequence 12250, A	c 210	14.8	74.0	33319	7	US-10-990-328A-97686	Sequence 97686, A
138	15.2	76.0	101813	7	US-10-990-328A-94049	Sequence 94049, A	c 211	14.8	74.0	43794	1	PCT-US04-31416-169	Sequence 169, App
139	15.2	76.0	133791	12	US-11-021-837-55	Sequence 55, Appl	c 212	14.8	74.0	45819	12	US-11-033-545-825	Sequence 825, App
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142	15.2	76.0	173354	1	PCT-US05-10257-330	Sequence 330, Appl	c 215	14.8	74.0	54542	7	US-10-990-328A-95235	Sequence 95235, A
143	15.2	76.0	228343	1	PCT-US04-31416-117	Sequence 117, App	c 216	14.8	74.0	54558	14	US-60-659-397-12104	Sequence 12104, A
144	15.2	76.0	232325	7	US-10-990-328A-94155	Sequence 94155, A	c 217	14.8	74.0	54762	14	US-60-659-397-12278	Sequence 12278, A
c 145	15.2	76.0	1391915	7	US-10-990-328A-94753	Sequence 94753, A	c 218	14.8	74.0	54794	7	US-10-990-328A-94602	Sequence 94602, A
146	15	75.0	19	9	US-10-923-516-114	Sequence 114, App	c 219	14.8	74.0	58080	7	US-10-990-328A-95792	Sequence 95792, A
c 147	15	75.0	19	8	US-10-923-516-528	Sequence 528, App	c 220	14.8	74.0	64392	7	US-10-990-328A-97019	Sequence 97019, A
c 148	15	75.0	22	8	US-10-605-923-1202679	Sequence 1202679, A	c 221	14.8	74.0	65001	14	US-60-649-586-99	Sequence 99, Appl
149	15	75.0	172543	11	US-11-121-086-6	Sequence 6, Appl	c 222	14.8	74.0	67997	7	US-10-990-328A-97148	Sequence 97148, A
150	15	75.0	191091	11	US-11-121-086-60	Sequence 60, Appl	c 223	14.8	74.0	79749	14	US-60-659-397-12106	Sequence 12106, A
151	14.8	74.0	23	8	US-10-604-985-51543	Sequence 51543, A	c 224	14.8	74.0	80577	7	US-10-990-328A-95237	Sequence 95237, A
152	14.8	74.0	25	11	US-11-121-0849-119795	Sequence 119795, A	c 225	14.8	74.0	121702	7	US-10-990-328A-97724	Sequence 97724, A
153	14.8	74.0	25	12	US-11-036-317-72317	Sequence 72317, A	c 226	14.8	74.0	145485	7	US-10-990-328A-95389	Sequence 95389, A
154	14.8	74.0	25	12	US-11-036-317-364556	Sequence 364556, A	c 227	14.8	74.0	149878	7	US-10-990-328A-95831	Sequence 95831, A
c 155	14.8	74.0	25	12	US-11-036-317-610702	Sequence 610702, A	c 228	14.8	74.0	166273	7	US-10-990-328A-96659	Sequence 96659, A
156	14.8	74.0	29	12	US-11-016-518A-5	Sequence 5, Appl	c 229	14.8	74.0	207600	11	US-11-112-908-31	Sequence 31, Appl
c 157	14.8	74.0	29	12	US-11-016-518A-6	Sequence 6, Appl	c 230	14.8	74.0	52949	7	US-10-990-328A-94135	Sequence 94135, A
158	14.8	74.0	118	12	US-11-021-493A-605	Sequence 605, App	c 231	14.8	74.0	2089378	9	US-10-526-324-1	Sequence 1, Appl
159	14.8	74.0	201	7	US-10-990-328A-316598	Sequence 316598, A	c 232	14.8	74.0	2089378	9	US-10-526-324-342	Sequence 342, App
c 160	14.8	74.0	201	7	US-10-990-328A-520426	Sequence 520426, A	c 233	14.8	74.0	2089378	9	US-10-526-324-723	Sequence 723, App
c 161	14.8	74.0	201	7	US-10-990-328A-541438	Sequence 541438, A	c 234	14.8	74.0	2089378	9	US-10-526-324-1087	Sequence 1087, App
162	14.8	74.0	201	14	US-60-659-397-30788	Sequence 30788, A	c 235	14.8	74.0	2089378	9	US-10-526-324-1469	Sequence 1469, App
163	14.8	74.0	291	9	US-10-991-218-613	Sequence 613, App	c 236	14.8	74.0	2089378	9	US-10-526-324-1838	Sequence 1838, App
164	14.8	74.0	425	9	US-10-703-032-53566	Sequence 53566, A	c 237	14.8	74.0	4830849	2	PCT-IB03-06509-1355	Sequence 1355, App
c 165	14.8	74.0	497	12	US-11-055-822-735	Sequence 735, App	c 238	14.4	72.0	19	2	PCT-US03-36787-137149	Sequence 137149, A

239	14.4	72.0	19	2	PCT-US03-36787-1371767	Sequence 1371767, A	312	14.4	72.0	16009	1	PCT-US05-00300-28	Sequence 28, Appl
240	14.4	72.0	19	10	US-10-714-3338-1371749	Sequence 1371749, A	313	14.4	72.0	17130	14	US-60-647-642-12	Sequence 12, Appl
241	14.4	72.0	19	10	US-10-714-3338-1371767	Sequence 1371767, A	314	14.4	72.0	17901	7	US-10-990-328A-97628	Sequence 97628, A
242	14.4	72.0	19	13	US-11-083-784-1371749	Sequence 1371749, A	315	14.4	72.0	18217	14	US-60-655-875-31	Sequence 31, Appl
243	14.4	72.0	19	13	US-11-083-784-1371767	Sequence 1371767, A	316	14.4	72.0	18425	7	US-10-990-328A-97137	Sequence 97137, A
244	14.4	72.0	22	8	US-10-605-924-710695	Sequence 710695, A	317	14.4	72.0	20202	7	US-10-990-328A-98241	Sequence 98241, A
245	14.4	72.0	23	8	US-10-605-923-1308644	Sequence 1308644, A	318	14.4	72.0	20202	7	US-10-990-328A-98309	Sequence 98309, A
246	14.4	72.0	23	8	US-10-605-923-1476528	Sequence 1476528, A	319	14.4	72.0	21287	12	US-11-073-360-1601	Sequence 1601, Ap
247	14.4	72.0	23	9	US-10-605-924-815823	Sequence 815823, A	320	14.4	72.0	22131	7	US-10-990-328A-94882	Sequence 94882, A
248	14.4	72.0	23	9	US-10-605-924-1103457	Sequence 1103457, A	321	14.4	72.0	22131	7	US-10-990-328A-96578	Sequence 96578, A
249	14.4	72.0	26	9	US-10-605-923-1476619	Sequence 1476619, A	322	14.4	72.0	27069	12	US-11-073-360-1602	Sequence 1602, Ap
250	14.4	72.0	26	9	US-10-605-924-815860	Sequence 815860, A	323	14.4	72.0	27239	7	US-60-660-591-32	Sequence 32, Appl
251	14.4	72.0	201	7	US-10-990-328A-154278	Sequence 154278, A	324	14.4	72.0	27239	7	US-10-990-328A-98243	Sequence 98243, A
252	14.4	72.0	201	7	US-10-990-328A-278940	Sequence 278940, A	325	14.4	72.0	28918	11	US-11-097-143-18925	Sequence 18925, A
253	14.4	72.0	201	7	US-10-990-328A-278941	Sequence 278941, A	326	14.4	72.0	31204	7	US-10-990-328A-98249	Sequence 98249, A
254	14.4	72.0	201	7	US-10-990-328A-278942	Sequence 278942, A	327	14.4	72.0	38287	7	US-10-990-328A-98212	Sequence 98212, A
255	14.4	72.0	201	7	US-10-990-328A-278943	Sequence 278943, A	328	14.4	72.0	40311	7	US-10-990-328A-95773	Sequence 95773, A
256	14.4	72.0	201	7	US-10-990-328A-340170	Sequence 340170, A	329	14.4	72.0	40678	7	US-10-990-328A-95413	Sequence 95413, A
257	14.4	72.0	201	7	US-10-990-328A-365318	Sequence 365318, A	330	14.4	72.0	42979	11	US-11-097-143-28946	Sequence 28946, A
258	14.4	72.0	201	7	US-10-990-328A-365345	Sequence 365345, A	331	14.4	72.0	43208	7	US-10-990-328A-95675	Sequence 95675, A
259	14.4	72.0	201	7	US-10-990-328A-409835	Sequence 409835, A	332	14.4	72.0	45088	7	US-10-990-328A-94389	Sequence 94389, A
260	14.4	72.0	201	7	US-10-990-328A-447318	Sequence 447318, A	333	14.4	72.0	48320	7	US-10-990-328A-94344	Sequence 94344, A
261	14.4	72.0	201	7	US-10-990-328A-484320	Sequence 484320, A	334	14.4	72.0	52177	7	US-10-990-328A-95672	Sequence 95672, A
262	14.4	72.0	201	7	US-10-990-328A-484321	Sequence 484321, A	335	14.4	72.0	57022	7	US-10-990-328A-94529	Sequence 94529, A
263	14.4	72.0	201	7	US-10-990-328A-485769	Sequence 485769, A	336	14.4	72.0	69819	7	US-10-990-328A-96148	Sequence 96148, A
264	14.4	72.0	201	7	US-10-990-328A-485966	Sequence 485966, A	337	14.4	72.0	82472	7	US-10-990-328A-93635	Sequence 93635, A
265	14.4	72.0	201	7	US-10-990-328A-486634	Sequence 486634, A	338	14.4	72.0	82637	7	US-10-990-328A-97218	Sequence 97218, A
266	14.4	72.0	201	7	US-10-990-328A-486732	Sequence 486732, A	339	14.4	72.0	86899	7	US-10-990-328A-93617	Sequence 93617, A
267	14.4	72.0	201	7	US-10-990-328A-516702	Sequence 516702, A	340	14.4	72.0	91462	7	US-10-990-328A-96290	Sequence 96290, A
268	14.4	72.0	201	7	US-10-990-328A-520487	Sequence 520487, A	341	14.4	72.0	99335	7	US-10-990-328A-97965	Sequence 97965, A
269	14.4	72.0	489	9	US-10-703-032-85274	Sequence 85274, A	342	14.4	72.0	113108	7	US-10-990-328A-94128	Sequence 94128, A
270	14.4	72.0	600	9	US-10-972-079-38998	Sequence 38998, A	343	14.4	72.0	121702	7	US-10-990-328A-97724	Sequence 97724, A
271	14.4	72.0	600	9	US-10-972-079-44848	Sequence 44848, A	344	14.4	72.0	137456	7	US-10-990-328A-94575	Sequence 94575, A
272	14.4	72.0	600	9	US-10-972-079-44849	Sequence 44849, A	345	14.4	72.0	142605	11	US-11-121-086-64	Sequence 64, Appl
273	14.4	72.0	600	9	US-10-972-079-74154	Sequence 74154, A	346	14.4	72.0	169725	11	US-11-121-086-63	Sequence 63, Appl
274	14.4	72.0	600	9	US-10-972-079-91154	Sequence 91154, A	347	14.4	72.0	179777	11	US-11-121-086-106	Sequence 106, App
275	14.4	72.0	600	9	US-10-972-079-91155	Sequence 91155, A	348	14.4	72.0	199289	7	US-10-990-328A-94296	Sequence 94296, A
276	14.4	72.0	600	9	US-10-972-079-91156	Sequence 91156, A	349	14.4	72.0	212474	11	US-11-121-086-10	Sequence 10, Appl
277	14.4	72.0	634	8	US-10-450-763-16441	Sequence 16441, A	350	14.4	72.0	212474	7	US-10-990-328A-97200	Sequence 97200, A
278	14.4	72.0	642	14	US-60-655-875-80365	Sequence 80365, A	351	14.4	72.0	217623	11	US-11-112-908-33	Sequence 33, Appl
279	14.4	72.0	777	9	US-10-703-032-76031	Sequence 76031, A	352	14.4	72.0	258463	14	US-60-659-397-11967	Sequence 11967, A
280	14.4	72.0	803	11	US-11-090-997-2740	Sequence 2740, Ap	353	14.4	72.0	258463	7	US-10-990-328A-93926	Sequence 93926, A
281	14.4	72.0	807	14	US-60-655-875-52408	Sequence 52408, A	354	14.4	72.0	336252	7	US-10-990-328A-97217	Sequence 97217, A
282	14.4	72.0	865	14	US-60-655-875-50791	Sequence 50791, A	355	14.4	72.0	474412	7	US-10-990-328A-98016	Sequence 98016, A
283	14.4	72.0	867	14	US-60-655-875-82755	Sequence 82755, A	356	14.4	72.0	738017	8	US-10-990-328A-96711	Sequence 96711, A
284	14.4	72.0	1067	14	US-60-655-875-7425	Sequence 7425, A	357	14.4	72.0	738017	8	US-10-605-924-658698	Sequence 658698, A
285	14.4	72.0	1106	8	US-10-450-763-29049	Sequence 29049, A	358	14.2	71.0	22	8	US-10-605-924-707651	Sequence 707651, A
286	14.4	72.0	1158	14	US-60-655-875-56683	Sequence 56683, A	359	14.2	71.0	24	8	US-10-605-923-52469	Sequence 52469, A
287	14.4	72.0	1470	8	US-10-450-763-1010	Sequence 1010, Ap	360	14.2	71.0	24	8	US-10-605-924-35974	Sequence 35974, A
288	14.4	72.0	1556	12	US-11-055-822-697	Sequence 697, App	361	14.2	71.0	25	12	US-11-036-317-135666	Sequence 135666, A
289	14.4	72.0	1578	9	US-10-703-032-23853	Sequence 23853, A	362	14.2	71.0	25	12	US-11-036-317-431849	Sequence 431849, A
290	14.4	72.0	1688	14	US-60-655-875-17219	Sequence 17219, A	363	14.2	71.0	25	12	US-11-036-317-973731	Sequence 973731, A
291	14.4	72.0	1790	8	US-10-450-763-4763	Sequence 4763, Ap	364	14.2	71.0	71	8	US-10-605-923-25326	Sequence 25326, A
292	14.4	72.0	1960	9	US-10-703-032-11047	Sequence 11047, A	365	14.2	71.0	71	8	US-10-605-924-17425	Sequence 17425, A
293	14.4	72.0	2054	14	US-60-655-875-25913	Sequence 25913, A	366	14.2	71.0	105	8	US-10-605-923-22393	Sequence 22393, A
294	14.4	72.0	2080	2	PCT-US04-42189-130	Sequence 130, App	367	14.2	71.0	105	8	US-10-605-924-15373	Sequence 15373, A
295	14.4	72.0	2167	14	US-60-655-875-18172	Sequence 18172, A	368	14.2	71.0	201	7	US-10-990-328A-119282	Sequence 119282, A
296	14.4	72.0	2182	2	PCT-US04-42189-9	Sequence 9, Appli	369	14.2	71.0	201	7	US-10-990-328A-212717	Sequence 212717, A
297	14.4	72.0	2373	11	US-11-097-143-31835	Sequence 31835, A	370	14.2	71.0	201	7	US-10-990-328A-231009	Sequence 231009, A
298	14.4	72.0	2537	8	US-10-450-763-35877	Sequence 35877, A	371	14.2	71.0	201	7	US-10-990-328A-231160	Sequence 231160, A
299	14.4	72.0	2578	7	US-10-990-328A-7057	Sequence 7057, Ap	372	14.2	71.0	201	7	US-10-990-328A-257119	Sequence 257119, A
300	14.4	72.0	2584	7	US-10-990-328A-7058	Sequence 7058, Ap	373	14.2	71.0	201	7	US-10-990-328A-263580	Sequence 263580, A
301	14.4	72.0	3074	14	US-60-655-875-21793	Sequence 21793, A	374	14.2	71.0	201	7	US-10-990-328A-263765	Sequence 263765, A
302	14.4	72.0	3568	14	US-60-655-875-16011	Sequence 16011, A	375	14.2	71.0	201	7	US-10-990-328A-266244	Sequence 266244, A
303	14.4	72.0	5442	11	US-11-097-143-31834	Sequence 31834, A	376	14.2	71.0	201	7	US-10-990-328A-293329	Sequence 293329, A
304	14.4	72.0	6266	9	US-10-955-0544-24	Sequence 24, Appl	377	14.2	71.0	201	7	US-10-990-328A-293905	Sequence 293905, A
305	14.4	72.0	8277	11	US-11-097-143-24844	Sequence 24844, A	378	14.2	71.0	201	7	US-10-990-328A-424080	Sequence 424080, A
306	14.4	72.0	8595	2	PCT-US05-03880-16	Sequence 16, Appl	379	14.2	71.0	201	7	US-10-990-328A-522376	Sequence 522376, A
307	14.4	72.0	10394	2	PCT-US04-00429-15	Sequence 15, Appl	380	14.2	71.0	201	12	US-11-073-360-14774	Sequence 14774, A
308	14.4	72.0	11355	14	US-60-669-529-18	Sequence 18, Appl	381	14.2	71.0	201	14	US-60-660-322-23857	Sequence 23857, A
309	14.4	72.0	13197	7	US-10-990-328A-96445	Sequence 96445, A	382	14.2	71.0	311	12	US-11-041-914-787	Sequence 787, App
310	14.4	72.0	13792	7	US-10-990-328A-96230	Sequence 96230, A	383	14.2	71.0	370	9	US-10-703-032-66123	Sequence 66123, A
311	14.4	72.0	13858	7	US-10-990-328A-94064	Sequence 94064, A	384	14.2	71.0	377	9	US-10-703-032-59158	Sequence 59158, A

C 531	14.2	71.0	4110	11	US-11-097-143-7804	Sequence 7804, Ap	C 504	14.2	71.0	88873	7	US-10-990-328A-93397	Sequence 93397, A
C 532	14.2	71.0	4352	10	US-10-531-164-483	Sequence 483, Ap	605	14.2	71.0	94825	7	US-10-990-328A-97905	Sequence 97905, A
C 533	14.2	71.0	4491	11	US-11-097-143-2824	Sequence 2824, Ap	606	14.2	71.0	100097	10	US-10-960-414-203	Sequence 203, App
C 534	14.2	71.0	4519	14	US-60-655-875-73471	Sequence 73471, A	C 607	14.2	71.0	100097	10	US-10-960-414-203	Sequence 203, App
C 535	14.2	71.0	4911	11	US-11-097-143-13502	Sequence 13502, A	C 608	14.2	71.0	104596	7	US-10-990-328A-95888	Sequence 95888, A
C 536	14.2	71.0	5043	11	US-11-099-266-70	Sequence 70, Appl	C 609	14.2	71.0	110577	7	US-10-990-328A-94468	Sequence 94468, A
C 537	14.2	71.0	5119	11	US-11-108-288-81	Sequence 81, Appl	C 610	14.2	71.0	112613	7	US-10-990-328A-97760	Sequence 97760, A
C 538	14.2	71.0	5249	14	US-60-664-582-1314	Sequence 1314, Ap	C 611	14.2	71.0	115995	14	US-60-659-397-12097	Sequence 12097, A
C 539	14.2	71.0	5322	14	US-60-655-875-10306	Sequence 10306, Ap	C 612	14.2	71.0	124972	11	US-11-121-086-100	Sequence 100, App
C 540	14.2	71.0	5399	14	US-60-655-875-1148	Sequence 1148, Ap	C 613	14.2	71.0	131860	12	US-11-033-545-730	Sequence 730, App
C 541	14.2	71.0	5634	14	US-60-655-875-78386	Sequence 78386, A	C 614	14.2	71.0	134174	11	US-11-121-086-99	Sequence 99, Appl
C 542	14.2	71.0	5783	10	US-10-531-164-487	Sequence 487, App	C 615	14.2	71.0	134561	7	US-10-990-328A-95282	Sequence 95282, A
C 543	14.2	71.0	5842	14	US-60-655-875-4771	Sequence 4771, Ap	C 616	14.2	71.0	145177	7	US-10-990-328A-93496	Sequence 93496, A
C 544	14.2	71.0	5879	14	US-60-660-851-78	Sequence 78, Appl	C 617	14.2	71.0	151031	7	US-10-990-328A-97759	Sequence 97759, A
C 545	14.2	71.0	6271	11	US-11-097-143-32584	Sequence 32584, A	C 618	14.2	71.0	158405	11	US-11-099-266-86	Sequence 86, Appl
C 546	14.2	71.0	6746	10	US-10-960-414-435	Sequence 435, App	C 619	14.2	71.0	161323	11	US-10-990-328A-94088	Sequence 94088, A
C 547	14.2	71.0	6786	11	US-11-097-143-25859	Sequence 25859, A	C 620	14.2	71.0	161994	11	US-11-112-908-57	Sequence 57, Appl
C 548	14.2	71.0	6997	14	US-60-655-875-2190	Sequence 2190, Ap	C 621	14.2	71.0	170837	11	US-11-121-086-97	Sequence 97, Appl
C 549	14.2	71.0	7503	9	US-10-270-333A-58	Sequence 58, Appl	C 622	14.2	71.0	175100	11	US-11-121-086-21	Sequence 21, Appl
C 550	14.2	71.0	7503	11	US-11-097-143-14635	Sequence 14635, A	C 623	14.2	71.0	181172	11	US-11-121-086-41	Sequence 41, Appl
C 551	14.2	71.0	7886	11	US-11-097-143-13501	Sequence 13501, A	C 624	14.2	71.0	185765	12	US-11-033-545-674	Sequence 674, App
C 552	14.2	71.0	8056	1	PCT-US05-14668-10	Sequence 10, Appl	C 625	14.2	71.0	185766	12	US-11-033-545-707	Sequence 707, App
C 553	14.2	71.0	8177	9	US-10-287-436A-673	Sequence 673, App	C 626	14.2	71.0	191331	11	US-11-112-908-20	Sequence 20, Appl
C 554	14.2	71.0	8747	9	US-10-955-054A-141	Sequence 141, App	C 627	14.2	71.0	193789	11	US-11-112-908-55	Sequence 55, Appl
C 555	14.2	71.0	9136	1	PCT-US05-11532-434	Sequence 434, App	C 628	14.2	71.0	200000	1	PCT-US04-37513-1	Sequence 1, Appl
C 556	14.2	71.0	9136	1	PCT-US05-11532-1038	Sequence 1038, Ap	C 629	14.2	71.0	207908	10	US-11-112-908-21	Sequence 21, Appl
C 557	14.2	71.0	9136	2	PCT-US04-42360-1772	Sequence 1772, Ap	C 630	14.2	71.0	223724	14	US-60-660-322-2245	Sequence 2245, Ap
C 558	14.2	71.0	10285	10	US-10-050-898A-283	Sequence 283, App	C 631	14.2	71.0	227189	7	US-10-990-328A-94743	Sequence 94743, A
C 559	14.2	71.0	10385	11	US-11-097-143-16558	Sequence 16558, A	C 632	14.2	71.0	262948	7	US-10-990-328A-93680	Sequence 93680, A
C 560	14.2	71.0	10568	11	PCT-US05-10257-903	Sequence 903, App	C 633	14.2	71.0	287803	7	US-60-659-397-11905	Sequence 11905, A
C 561	14.2	71.0	10807	11	US-11-097-143-16537	Sequence 16537, A	C 634	14.2	71.0	287819	14	US-10-990-328A-94956	Sequence 94956, A
C 562	14.2	71.0	11394	11	US-11-097-143-25858	Sequence 25858, A	C 635	14.2	71.0	300311	7	PCT-US05-14965-376	Sequence 376, App
C 563	14.2	71.0	12146	14	US-60-660-590-88	Sequence 88, Appl	C 636	14.2	71.0	330354	1	PCT-US05-14965-364	Sequence 364, App
C 564	14.2	71.0	12967	7	US-10-990-328A-93330	Sequence 93330, A	C 637	14.2	71.0	350878	7	US-10-990-328A-95035	Sequence 95035, A
C 565	14.2	71.0	15969	7	US-10-990-328A-97816	Sequence 97816, A	C 638	14.2	71.0	353669	7	US-11-029-984-1	Sequence 1, Appl
C 566	14.2	71.0	16516	7	US-10-990-328A-97631	Sequence 97631, A	C 639	14.2	71.0	382259	11	US-10-990-328A-97318	Sequence 97318, A
C 567	14.2	71.0	16726	12	US-11-073-360-1638	Sequence 1638, Ap	C 640	14.2	71.0	415117	7	US-10-990-328A-96177	Sequence 96177, A
C 568	14.2	71.0	20145	14	US-60-659-397-12126	Sequence 12126, A	C 641	14.2	71.0	415117	7	US-10-990-328A-96177	Sequence 96177, A
C 569	14.2	71.0	22619	7	US-10-990-328A-96857	Sequence 96857, A	C 642	14.2	71.0	430873	7	US-10-990-328A-96177	Sequence 96177, A
C 570	14.2	71.0	23794	7	US-10-990-328A-93361	Sequence 93361, A	C 643	14.2	71.0	462586	9	US-10-476-264-420	Sequence 420, App
C 571	14.2	71.0	23222	7	US-10-990-328A-95924	Sequence 95924, A	C 644	14.2	71.0	652661	7	US-10-990-328A-97235	Sequence 97235, A
C 572	14.2	71.0	23351	7	US-10-990-328A-94893	Sequence 94893, A	C 645	14.2	71.0	961710	7	US-10-990-328A-94469	Sequence 94469, A
C 573	14.2	71.0	23738	12	US-11-031-175-1203	Sequence 1203, Ap	C 646	14.2	71.0	961710	7	US-10-990-328A-94469	Sequence 94469, A
C 574	14.2	71.0	28054	1	PCT-US05-10257-700	Sequence 700, App	C 647	14.2	71.0	1316554	14	US-60-660-322-2241	Sequence 2241, Ap
C 575	14.2	71.0	28244	7	US-10-990-328A-97317	Sequence 97317, A	C 648	14.2	71.0	1691139	9	US-10-868-397-1	Sequence 1, Appl
C 576	14.2	71.0	31664	7	US-10-990-328A-95922	Sequence 95922, A	C 649	14.2	71.0	1691140	9	US-10-868-397-1	Sequence 1, Appl
C 577	14.2	71.0	31737	7	US-10-990-328A-97799	Sequence 97799, A	C 650	14.2	71.0	1980090	7	US-10-990-328A-97595	Sequence 97595, A
C 578	14.2	71.0	34552	12	US-11-031-175-1262	Sequence 1262, Ap	C 651	14	70.0	25	9	US-10-932-182A-86155	Sequence 86155, A
C 579	14.2	71.0	35073	7	US-10-990-328A-94077	Sequence 94077, A	C 652	14	70.0	25	12	US-11-060-756-182708	Sequence 182708, A
C 580	14.2	71.0	37145	7	US-10-990-328A-96078	Sequence 96078, A	C 653	14	70.0	25	12	US-11-060-756-182709	Sequence 182709, A
C 581	14.2	71.0	39303	7	US-10-990-328A-97967	Sequence 97967, A	C 654	14	70.0	25	12	US-11-060-756-209315	Sequence 209315, A
C 582	14.2	71.0	40376	1	PCT-US05-14965-446	Sequence 446, App	C 655	14	70.0	201	7	US-10-990-328A-138298	Sequence 138298, A
C 583	14.2	71.0	42309	7	US-10-990-328A-97438	Sequence 97438, A	C 656	14	70.0	201	7	US-10-990-328A-138300	Sequence 138300, A
C 584	14.2	71.0	42380	7	US-10-990-328A-94638	Sequence 94638, A	C 657	14	70.0	201	7	US-10-990-328A-138335	Sequence 138335, A
C 585	14.2	71.0	43704	7	US-10-990-328A-97047	Sequence 97047, A	C 658	14	70.0	201	7	US-10-990-328A-138340	Sequence 138340, A
C 586	14.2	71.0	43778	7	US-10-990-328A-96324	Sequence 96324, A	C 659	14	70.0	201	7	US-10-990-328A-208891	Sequence 208891, A
C 587	14.2	71.0	49225	12	US-11-031-175-1269	Sequence 1269, Ap	C 660	14	70.0	201	7	US-10-990-328A-278234	Sequence 278234, A
C 588	14.2	71.0	49252	7	US-10-990-328A-93907	Sequence 93907, A	C 661	14	70.0	201	7	US-10-990-328A-516698	Sequence 516698, A
C 589	14.2	71.0	50053	7	US-10-990-328A-95864	Sequence 95864, A	C 662	14	70.0	201	14	US-60-659-397-9219	Sequence 9219, Ap
C 590	14.2	71.0	57336	7	US-10-990-328A-97065	Sequence 97065, A	C 663	14	70.0	201	14	US-60-659-397-36175	Sequence 36175, A
C 591	14.2	71.0	59289	7	US-10-990-328A-94348	Sequence 94348, A	C 664	14	70.0	487	9	US-10-703-032-53454	Sequence 53454, A
C 592	14.2	71.0	59206	7	US-10-990-328A-94326	Sequence 94326, A	C 665	14	70.0	600	9	US-10-972-079-27726	Sequence 27726, A
C 593	14.2	71.0	61486	7	US-10-990-328A-94416	Sequence 94416, A	C 666	14	70.0	600	9	US-10-972-079-27727	Sequence 27727, A
C 594	14.2	71.0	65992	7	US-10-990-328A-96345	Sequence 96345, A	C 667	14	70.0	600	12	US-11-060-756-2335	Sequence 2335, Ap
C 595	14.2	71.0	76003	7	US-10-990-328A-94217	Sequence 94217, A	C 668	14	70.0	600	12	US-11-060-756-2336	Sequence 2336, Ap
C 596	14.2	71.0	73208	7	US-10-990-328A-94249	Sequence 94249, A	C 669	14	70.0	600	12	US-11-060-756-2336	Sequence 2336, Ap
C 597	14.2	71.0	74545	12	US-11-033-545-606	Sequence 606, App	C 670	14	70.0	600	12	US-11-060-756-6608	Sequence 6608, Ap
C 598	14.2	71.0	75426	7	US-10-990-328A-93254	Sequence 93254, A	C 671	14	70.0	626	9	US-10-703-032-73119	Sequence 73119, A
C 599	14.2	71.0	78029	7	US-10-990-328A-94687	Sequence 94687, A	C 672	14	70.0	733	1	PCT-US05-00517-933	Sequence 933, App
C 600	14.2	71.0	78237	7	US-10-990-328A-94852	Sequence 94852, A	C 673	14	70.0	737	1	PCT-US05-10257-285	Sequence 285, App
C 601	14.2	71.0	79122	11	US-11-117-187-200	Sequence 200, App	C 674	14	70.0	1085	14	US-60-655-875-79111	Sequence 79111, A
C 602	14.2	71.0	83493	2	PCT-US03-41242-61	Sequence 61, Appl	C 675	14	70.0	1113	9	US-10-932-182A-75641	Sequence 75641, A
C 603	14.2	71.0	88873	7	US-10-990-328A-93397	Sequence 93397, A	C 676	14	70.0	1386	8	US-10-450-763-10633	Sequence 10633, A

Query Match 100.0%; Score 20; DB 9; Length 717;
Best Local Similarity 80.0%; Pred. No. 9.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAUGCCUU 20
|||||||:|||||:|||||:
Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 3

PCT-US04-43454-1706
; Sequence 1706, Application PC/TUS0443454
; GENERAL INFORMATION:
; APPLICANT: THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
; APPLICANT: REICH, SAMUEL JOTHAM
; APPLICANT: TOLENTINO, MICHAEL J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE
; FILE REFERENCE: DBR-04-1324PCT
; CURRENT APPLICATION NUMBER: PCT/US04/43454
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,099
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 1733
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1706
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(703)
PCT-US04-43454-1706

Query Match 100.0%; Score 20; DB 2; Length 741;
Best Local Similarity 80.0%; Pred. No. 9.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAUGCCUU 20
|||||||:|||||:|||||:
Db 566 AACGGAGGCTGGGATGCCTT 585

RESULT 4

PCT-US04-43454-1704
; Sequence 1704, Application PC/TUS0443454
; GENERAL INFORMATION:
; APPLICANT: THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
; APPLICANT: REICH, SAMUEL JOTHAM
; APPLICANT: TOLENTINO, MICHAEL J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE
; FILE REFERENCE: DBR-04-1324PCT
; CURRENT APPLICATION NUMBER: PCT/US04/43454
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,099
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 1733
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1704
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(775)
PCT-US04-43454-1704

Query Match 100.0%; Score 20; DB 2; Length 777;
Best Local Similarity 80.0%; Pred. No. 9.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAUGCCUU 20
|||||||:|||||:|||||:
Db 602 AACGGAGGCTGGGATGCCTT 621

RESULT 5

US-10-961-458-19
; Sequence 19, Application US/10961458
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
; FILE REFERENCE: 04040/1200990-US7
; CURRENT APPLICATION NUMBER: US/10/961,458
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US/10/961,458
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US 09/375,514
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 09/080,285
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: US 08/455,485
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/124,256
; PRIOR FILING DATE: 1993-09-20
; PRIOR APPLICATION NUMBER: US 07/840,716
; PRIOR FILING DATE: 1992-02-21
; PRIOR APPLICATION NUMBER: US 07/288,692
; PRIOR FILING DATE: 1988-12-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 5086
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-961-458-19

Query Match 100.0%; Score 20; DB 9; Length 5086;
Best Local Similarity 80.0%; Pred. No. 9.4;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAUGCCUU 20
|||||||:|||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 6

US-10-887-066-1
; Sequence 1, Application US/10887066
; GENERAL INFORMATION:
; APPLICANT: Chen, Dong Feng et al.
; TITLE OF INVENTION: Methods and compositions for promoting axon regeneration and cell
; FILE REFERENCE: ERM-106.01
; CURRENT APPLICATION NUMBER: US/10/887,066
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)..(751)
US-10-887-066-1

Query Match 100.0%; Score 20; DB 9; Length 6030;
Best Local Similarity 80.0%; Pred. No. 9.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAUGCCUU 20
|||||||:|||||:|||||:
Db 605 AACGGAGGCTGGGATGCCTT 624

RESULT 7

```
US-60-659-397-671
; Sequence 671, Application US/60659397
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/659,397
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 671
; LENGTH: 6145
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-659-397-671

Query Match      100.0%; Score 20; DB 14; Length 6145;
Best Local Similarity 80.0%; Pred. No. 9.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
|||||:||||:||||:||||:
Db 720 AACGGAGGCTGGGATGCCTT 739

RESULT 8
US-10-990-328A-203044
; Sequence 203044, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203044
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-990-328A-203044

Query Match      92.0%; Score 18.4; DB 7; Length 201;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
|||||:||||:||||:||||:
Db 148 AACGTAGGCTGGGATGCCTT 167

RESULT 9
US-10-990-328A-94275
; Sequence 94275, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94275
; LENGTH: 665590
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(665590)
; OTHER INFORMATION: n = A,T,C or G
US-10-990-328A-94275

Query Match      92.0%; Score 18.4; DB 7; Length 665590;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
|||||:||||:||||:||||:
Db 488568 AACGTAGGCTGGGATGCCTT 488587

RESULT 10
US-10-941-663A-247
; Sequence 247, Application US/10941663A
; GENERAL INFORMATION:
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF ANTI-APOPTO
; TITLE OF INVENTION: GENES
; FILE REFERENCE: 14174-105001
; CURRENT APPLICATION NUMBER: US/10/941,663A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: US 10/384,260
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00151
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 247
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sense strand of dsRNA that is complementary to a
; OTHER INFORMATION: Sequence of the human Bcl-2 gene
US-10-941-663A-247

Query Match      90.0%; Score 18; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCC 18
|||||:||||:||||:||||:
Db 4 AACGGAGGCGUGGAUGCC 21

RESULT 11
US-10-941-663A-248/c
; Sequence 248, Application US/10941663A
; GENERAL INFORMATION:
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF ANTI-APOPTO
; TITLE OF INVENTION: GENES
; FILE REFERENCE: 14174-105001
; CURRENT APPLICATION NUMBER: US/10/941,663A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: US 10/384,260
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00151
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 248
; LENGTH: 23
; TYPE: RNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense strand of dsRNA that is complementary to a
; OTHER INFORMATION: Sequence of the human Bcl-2 gene
US-10-941-663A-248

Query Match          90.0%; Score 18; DB 10; Length 23;
Best Local Similarity 88.9%; Pred. No. 72;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTUGGGAUGCC 18
    |||||:||||:|
Db 18 AACGGAGGCTGGGATGCC 1

RESULT 12
US-10-450-763-19742/c
; Sequence 19742, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 19742
; LENGTH: 2779
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (980)..(1330)
; OTHER INFORMATION: 76% homologous to Homo sapiens Similar to KIAA0174 gene
; OTHER INFORMATION: product,accession number BC000430,Smith-Waterman Score=416.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2779)
; OTHER INFORMATION: n = a,t,c or g
US-10-450-763-19742

Query Match          87.0%; Score 17.4; DB 8; Length 2779;
Best Local Similarity 73.7%; Pred. No. 1.5e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ACGGAGGCGUGGAGCCUU 20
    |||||:||||:|
Db 1909 ACGGAGGCTGGGATGCTTT 1891

RESULT 13
US-10-941-663A-361
; Sequence 361, Application US/10941663A
; GENERAL INFORMATION:
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF ANTI-APOPTO
; FILE REFERENCE: 14174-105001
; CURRENT APPLICATION NUMBER: US/10/941,663A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: US 10/384,260
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00151
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 446
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 361
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sense strand of dsRNA that is complementary to a
; OTHER INFORMATION: Sequence of the human Bcl-2 gene
US-10-941-663A-361

Query Match          85.0%; Score 17; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGGAUGC 17
    |||||:||||:|
Db 5 AACGGAGGCGUGGGAUGC 21

RESULT 14
US-10-941-663A-362/c
; Sequence 362, Application US/10941663A
; GENERAL INFORMATION:
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF ANTI-APOPTO
; FILE REFERENCE: 14174-105001
; CURRENT APPLICATION NUMBER: US/10/941,663A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: US 10/384,260
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00151
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 362
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense strand of dsRNA that is complementary to a
; OTHER INFORMATION: Sequence of the human Bcl-2 gene
US-10-941-663A-362

Query Match          85.0%; Score 17; DB 10; Length 23;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGGAUGC 17
    |||||:||||:|
Db 17 AACGGAGGCTGGGATGC 1

RESULT 15
PCT-US04-43830-3
; Sequence 3, Application PC/TUS0443830
; GENERAL INFORMATION:
; APPLICANT: KALOBIOS, INC.
; TITLE OF INVENTION: TRANSACTIVATION SYSTEM FOR MAMMALIAN CELLS
; FILE REFERENCE: CELA-001/01 WO
; CURRENT APPLICATION NUMBER: PCT/US04/43830
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,917
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Cricetulus longicaudatus
PCT-US04-43830-3
```

```
Query Match      84.0%; Score 16.8; DB 1; Length 588;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
    |||||:||||:||||:|:|:|
Db 442 AACGGAGGCTGGGACGCATT 461

RESULT 16
PCT-US04-43830-45
; Sequence 45, Application PC/TUS0443830
; GENERAL INFORMATION:
; APPLICANT: KALOBIOS, INC.
; TITLE OF INVENTION: TRANSACTIVATION SYSTEM FOR MAMMALIAN CELLS
; CURRENT APPLICATION NUMBER: PCT/US04/43830
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,917
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 45
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Cricetus longicaudatus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(587)
PCT-US04-43830-45

Query Match      84.0%; Score 16.8; DB 1; Length 596;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
    |||||:||||:||||:|:|:|
Db 444 AACGGAGGCTGGGACGCATT 463

RESULT 17
US-11-097-143-38804
; Sequence 38804, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38804
; LENGTH: 2206

Query Match      84.0%; Score 16.8; DB 9; Length 3051;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-38804

Query Match      84.0%; Score 16.8; DB 11; Length 2206;
Best Local Similarity 70.0%; Pred. No. 2.8e+02;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
    |||||:||||:||||:|:|:|
Db 907 AACGGACGCTGGGATGGCTT 926

RESULT 18
US-10-489-448-205/c
; Sequence 205, Application US/10489448
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yunqing
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Dmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 810CIP PCT
; CURRENT APPLICATION NUMBER: US/10/489,448
; CURRENT FILING DATE: 1004-03-10
; PRIOR APPLICATION NUMBER: US 60/324,631
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3476
; SOFTWARE: pt FL_genes Version 6.0
; SEQ ID NO 205
; LENGTH: 3051
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (110)..(3001)
US-10-489-448-205

Query Match      84.0%; Score 16.8; DB 9; Length 3051;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 AACGAGGCTGGGGAUGCCUU 20
Db 2346 AACGAGGCTGGGAGGCTT 2327

RESULT 19
US-11-097-143-38803/c
; Sequence 3803, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38803
; LENGTH: 4206
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-38803

Query Match 84.0%; Score 16.8; DB 11; Length 4206;
Best Local Similarity 70.0%; Pred. No. 2.8e+02;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGAGGCTGGGGAUGCCUU 20
Db 2300 AACGAGGCTGGGATGGCTT 2281

RESULT 20
PCT-US04-31416-55/c
; Sequence 55, Application PC/TUS0431416
; GENERAL INFORMATION:
; APPLICANT: Chiron Corporation
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: CHIR0017-500 (PP023353.02)
; CURRENT APPLICATION NUMBER: PCT/US04/31416
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: US 10/670,914
; PRIOR FILING DATE: 2003-09-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 87331
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(87331)

; OTHER INFORMATION: n = A, T, C or G
PCT-US04-31416-55

Query Match 84.0%; Score 16.8; DB 1; Length 87331;
Best Local Similarity 75.0%; Pred. No. 3e+02;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGAGGCTGGGGAUGCCUU 20
Db 11321 AACTGAGCTGGGATGCCAT 11302

RESULT 21
PCT-US05-11532-807
; Sequence 807, Application PC/TUS0511532
; GENERAL INFORMATION:
; APPLICANT: Porter, Mark
; APPLICANT: Higgs, Brandon
; APPLICANT: Mendrick, Donna
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: HEPATOTOXICITY MOLECULAR MODELS
; FILE REFERENCE: 044921-5134-WO
; CURRENT APPLICATION NUMBER: PCT/US05/11532
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: US 60/559,949
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 2005
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 807
; LENGTH: 1910
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US05-11532-807

Query Match 80.0%; Score 16; DB 1; Length 1910;
Best Local Similarity 87.5%; Pred. No. 6.6e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ACGGAGCGCGGGAUGC 17
Db 1280 ACGGAGCGCTGGGATGC 1295

RESULT 22
US-11-059-535-2115
; Sequence 2115, Application US/11059535
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Castile, Arthur
; APPLICANT: Johnson, Kory
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-01-US
; CURRENT APPLICATION NUMBER: US/11/059,535
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/10/060,087
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/331,273
```

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, PRIOR FILING DATE: 2001-11-13
, PRIOR APPLICATION NUMBER: US 09/917,800
, PRIOR FILING DATE: 2001-07-31
, NUMBER OF SEQ ID NOS: 2534
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 2115
, LENGTH: 1910
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, OTHER INFORMATION: Genbank Accession N
US-11-059-535-2115

```

Query Match 80.0%; Score 16; DB 12; Length 1910;
Best Local Similarity 87.5%; Pred. No. 6.6e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

Query Match      79.0%; Score 15.8; DB 7; Length 201;
Best Local Similarity 73.%; Pred. NO. 7.8e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAUCCU 19
Db 55 ACCGGAGGCTGGGGTGCCT 37

```


Db 1330 AGGGGGCTGGGATGCCTT 1312

RESULT 31

US-11-097-143-19546/c
; Sequence 19546, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19546
; LENGTH: 2687
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-19546

Query Match 79.0%; Score 15.8; DB 11; Length 2687;
Best Local Similarity 78.9%; Pred. No. 8.2e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGGCGGAGCCU 19

Db 146 AACGGAGCGTGGGACGGCT 128

RESULT 32

US-60-655-875-14030
; Sequence 14030, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijing
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McGarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 14030
; LENGTH: 2746
; TYPE: DNA
; ORGANISM: Heterodera glycines
US-60-655-875-14030

Query Match 79.0%; Score 15.8; DB 14; Length 2746;
Best Local Similarity 68.4%; Pred. No. 8.2e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGCGGCGGAGCCUU 20

Db 992 AGGGGGCTGGGATGCCTT 1010

RESULT 33

US-11-097-143-19540/c
; Sequence 19540, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19540
; LENGTH: 3999
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-19540

Query Match 79.0%; Score 15.8; DB 11; Length 3999;
Best Local Similarity 78.9%; Pred. No. 8.3e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGGCGGAGCCU 19

Db 2378 AACGGAGCGTGGGACGGCT 2360

RESULT 34

US-10-990-328A-96429/c
; Sequence 96429, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96429
; LENGTH: 18957
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

Matches 13; Conservative 4; Mismatches 2

; CURRENT APPLICATION NUMBER: US/10/990.328A
 ; CURRENT FILING DATE: 2004-11-17
 ; NUMBER OF SEQ ID NOS: 558824
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 202031
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-990-328A-202031

Query Match 77.0%; Score 15.4; DB 7; Length 201;
 Best Local Similarity 76.5%; Pred. No. 1.2e+03;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 CGAGGCGUGGAUGCCU 19
 |||||:||||:|
 Db 47 CTGAGGCTGGGAGCCT 63

RESULT 45
 US-10-990-328A-214862
 ; Sequence 214862, Application US/10990328A
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
 ; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
 ; FILE REFERENCE: CL001495
 ; CURRENT APPLICATION NUMBER: US/10/990.328A
 ; CURRENT FILING DATE: 2004-11-17
 ; NUMBER OF SEQ ID NOS: 558824
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 214862
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-990-328A-214862

Query Match 77.0%; Score 15.4; DB 7; Length 201;
 Best Local Similarity 70.6%; Pred. No. 1.2e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 GGAGGCGUGGAUGCCU 20
 |||||:||||:|
 Db 135 GGAGGCTGGGCTGCTT 151

RESULT 46
 US-10-990-328A-355604
 ; Sequence 355604, Application US/10990328A
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
 ; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
 ; FILE REFERENCE: CL001495
 ; CURRENT APPLICATION NUMBER: US/10/990.328A
 ; CURRENT FILING DATE: 2004-11-17
 ; NUMBER OF SEQ ID NOS: 558824
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 355604
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-990-328A-355604

Query Match 77.0%; Score 15.4; DB 7; Length 201;
 Best Local Similarity 76.5%; Pred. No. 1.2e+03;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 GGAGGCGUGGAUGCCU 20
 |||||:||||:|
 Db 77 GGAGGCTGGGAGCCTT 93

RESULT 47
 US-10-990-328A-507450
 ; Sequence 507450, Application US/10990328A
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
 ; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
 ; FILE REFERENCE: CL001495
 ; CURRENT APPLICATION NUMBER: US/10/990.328A
 ; CURRENT FILING DATE: 2004-11-17
 ; NUMBER OF SEQ ID NOS: 558824
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 507450
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-990-328A-507450

Query Match 77.0%; Score 15.4; DB 7; Length 201;
 Best Local Similarity 76.5%; Pred. No. 1.2e+03;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 GGAGGCGUGGAUGCCU 20
 |||||:||||:|
 Db 58 GGAGGCTGGGAGCCTT 74

RESULT 48
 US-10-990-328A-507451
 ; Sequence 507451, Application US/10990328A
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
 ; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
 ; FILE REFERENCE: CL001495
 ; CURRENT APPLICATION NUMBER: US/10/990.328A
 ; CURRENT FILING DATE: 2004-11-17
 ; NUMBER OF SEQ ID NOS: 558824
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 507451
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-990-328A-507451

Query Match 77.0%; Score 15.4; DB 7; Length 201;
 Best Local Similarity 76.5%; Pred. No. 1.2e+03;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 GGAGGCGUGGAUGCCU 20
 |||||:||||:|
 Db 77 GGAGGCTGGGAGCCTT 93

RESULT 49
 US-10-972-079-57470
 ; Sequence 57470, Application US/10972079
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: KERR, Richard
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: HOLM, Tom
 ; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
 ; FILE REFERENCE: MM1110-2
 ; CURRENT APPLICATION NUMBER: US/10/972.079
 ; CURRENT FILING DATE: 2004-10-22

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/ PRIOR APPLICATION NUMBER: US 60/514,333
/ PRIOR FILING DATE: 2003-10-24
/ NUMBER OF SEQ ID NOS: 96631
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 57470
/ LENGTH: 599
/ TYPE: DNA
/ ORGANISM: Chicken 19866894313426_1
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(76)
/ OTHER INFORMATION: n is any nucleotide
US-10-972-079-57470

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Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db      473 CGCAGGCTGGGATGCCT 489

RESULT 50
US-10-972-079-34295/c
/ Sequence 34295, Application US/10972079
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: ROSENFELD, David
/ APPLICANT: KERR, Richard
/ APPLICANT: BATES, Stephen
/ APPLICANT: HOLM, Tom
/ TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEP
/ FILE REFERENCE: MM1110-2
/ CURRENT APPLICATION NUMBER: US/10/972,079
/ PRIOR FILING DATE: 2004-10-22
/ PRIOR APPLICATION NUMBER: US 60/514,333
/ PRIOR FILING DATE: 2003-10-24
/ NUMBER OF SEQ ID NOS: 96631
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US-10-972-079-34295

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Search completed: May 24, 2005, 08:33:47
Job time : 3963 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 07:26:19 ; Search time 1824 Seconds
(without alignments)
531.307 Million cell updates/sec

Title: US-10-018-437-2

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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3: gb_in.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 5	15.2	76.0	20	6	AX045384 Sequence
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C 9	13.8	69.0	48	6	AX611886 Sequence
C 10	13.6	68.0	30	6	AX047706 Sequence
C 11	13.6	68.0	38	6	I14138 Sequence
C 12	13.6	68.0	50	6	AR122087 Sequence
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REFERENCE
AUTHORS
TITLE
JOURNAL
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ACCESSION
AX045383
VERSION
AX045383.1 GI:11343867
KEYWORDS
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SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.

REFERENCE
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AUTHORS
Zangemeister-Wittke,U., Luedke,G. and Huesken,D.
TITLE
Oligonucleotide derivatives directed against human bcl-xl and human
bcl-2 mRNA
JOURNAL
Patent: WO 0066724-A 3 09-NOV-2000;
Universitaet Zuerich (CH)
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Sequence 5 from Patent WO0066724.
ACCESSION
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VERSION
AX045385.1 GI:11343869
KEYWORDS
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ORGANISM
other sequences; artificial sequences.

REFERENCE
1
AUTHORS
Zangemeister-Wittke,U., Luedke,G. and Huesken,D.
TITLE
Oligonucleotide derivatives directed against human bcl-xl and human
bcl-2 mRNA

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ALIGNMENTS

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LOCUS
DEFINITION
Sequence 2 from Patent WO0066724.
ACCESSION
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VERSION
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KEYWORDS
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ORGANISM
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11

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Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Aggarwal, B.B.
TITLE Uses of THANK, a TNF homologue that activates apoptosis
JOURNAL Patent: US 6475986-A 11 05-NOV-2002;
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Db 18 CCGAGGCTGGGATCCC 3
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DEFINITION Sequence 19 from patent US 6432408.
ACCESSION AR222802
VERSION AR222802.1 GI:23330510
KEYWORDS
SOURCE
ORGANISM
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    Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Meng, X.-J., Emerson, S.U. and Purcell, R.H.
TITLE Swine hepatitis E virus and uses thereof
JOURNAL Patent: US 6432408-A 19 13-AUG-2002;
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VERSION AX611886.1 GI:28407315
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REFERENCE 1
AUTHORS Cullen, P. and Seedorf, U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 2911 19-SEP-2002;
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    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hoogenboom, H.R., Reurs, A. and Beiboer, S.H.
TITLE Antibodies
JOURNAL Patent: WO 0069914-A 24 23-NOV-2000;
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ACCESSION I14138
VERSION I14138.1 GI:996561
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SOURCE
ORGANISM
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    Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Hammock, B.D., Grant, D.F. and Beetham, J.K.
TITLE Recombinant soluble epoxide hydrolase
JOURNAL Patent: US 5445956-A 12 29-AUG-1995;
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LOCUS AR122087 50 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 17 from patent US 6165477.
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ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 50)
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TITLE       Subunit immunogenic composition against dengue infection
JOURNAL     Patent: US 6165477-A 17 26-DEC-2000;
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ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Ivy, J., Nakano, E. and Clements, D.
TITLE       Methods of preparing carboxy-terminally truncated recombinant
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            expression systems
JOURNAL     Patent: US 6165477-A 17 26-DEC-2000;
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RESULT 14
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DEFINITION Synthetic construct DNA, forward primer for human STS sts-stSG10311
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ACCESSION   AB069408
VERSION     AB069408.1  GI:15130212
KEYWORDS
SOURCE      synthetic construct
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            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Chen, Y. Z., Hayaishi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
            Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
            Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.
            and Soeda, E.
TITLE       A BAC-based STS-content map spanning a 35-Mb region of human

chromosome lp35-p36
Genomics 74 (1), 55-70 (2001)
MEDLINE    21269192
PUBMED     11374902
REFERENCE   2 (bases 1 to 19)
AUTHORS     Horii, A.
TITLE       Direct Submission
JOURNAL     Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
            Tel: 81-22-717-8042, Fax: 81-22-717-8047)
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Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGGCGGGAUGCCUU 20
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Db 18 AGGCGGGAUGCCUU 4

RESULT 15
CQ005245/c
LOCUS       CQ005245              50 bp      DNA      linear      PAT 16-JAN-2004
DEFINITION Sequence 3885 from Patent WO0147944.
ACCESSION   CQ005245
VERSION     CQ005245.1  GI:41011877
KEYWORDS
SOURCE      Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shimkets, R. A. and Leach, M.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL     Patent: WO 0147944-A 3885 05-JUL-2001;
            Curagen Corporation (US)
FEATURES
  source    Location/Qualifiers
            1..50
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

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            Accession number cg44916647"

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Best Local Similarity 73.3%; Pred. No. 1.1e+05;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GAGCGGGAUGCCU 19
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Db 40 GATGCTGGATGCT 26

RESULT 16
AX164981/c
LOCUS       AX164981              50 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 176 from Patent WO0138586.
ACCESSION   AX164981
VERSION     AX164981.1  GI:14545810

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KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Shimkets, R.A. and Leach, M.
JOURNAL Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
AUTHORS Patent: WO 0138586-A 176 31-MAY-2001;
FEATURES Curagen Corporation (US)
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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notes="Nucleotide deleted between bases 25 and 26
Accession number cg4916647"
variation 26
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Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 5 GAGGCGGGAUGCCU 19
|||||:|||||:|:
Db 42 GATGCTGGGATGCCT 28
RESULT 17
AR124994/c
LOCUS AR124994 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 45 from patent US 6172216.
ACCESSION AR124994
VERSION AR124994.1 GI:14110355
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C. Frank., Dean, N. M., Monia, B. P., Nickoloff, B. J. and Zhang, Q.
TITLE Antisense modulation of BCL-X expression
JOURNAL Patent: US 6172216-A 45 09-JAN-2001;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 61.1%; Pred. No. 1.6e+05;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 CGGAGCGGGAUGCCUU 20
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Db 20 CGGCGCTGGGATCTTT 3
RESULT 18
AR144319/c
LOCUS AR144319 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 47 from patent US 6210892.
ACCESSION AR144319
VERSION AR144319.1 GI:15106186
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
Bennett, C. Frank., Cooke, S. T., Manoharan, M., Wyatt, J. R., Baker, B. P., Monia, B. P., Freier, S. M., McKay, R. and Karras, J. G.
TITLE Alteration of cellular behavior by antisense modulation of mRNA processing
JOURNAL Patent: US 6210892-A 47 03-APR-2001;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"
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Query Match 66.0%; Score 13.2; DB 6; Length 20;
Best Local Similarity 61.1%; Pred. No. 1.6e+05;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 CGGAGCGGGAUGCCUU 20
|||||:|||||:|:
Db 20 CGGCGCTGGGATCTTT 3
RESULT 19
BD243084/c
LOCUS BD243084 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of bcl-x expression.
ACCESSION BD243084
VERSION BD243084.1 GI:33052854
KEYWORDS JP 2002526093-A/43.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, F. C., Dean, N. M., Monia, B. P., Nickoloff, B. J. and Zhang, Q.
TITLE Antisense modulation of bcl-x expression
JOURNAL Patent: JP 2002526093-A 43 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526093-A/43
PD 20-AUG-2002
PF 28-SEP-1999 JP 2000574543
PR 07-OCT-1998 US 09/167921, 26-MAR-1999 US 09/277020 PR
PI FRANK C BENNETT, NICHOLAS M DEAN, BRETT P MONIA, BRIAN J PI
NICKOLOFF,
PI QINGQING ZHANG
PC C12N15/09, A61K31/337, A61K31/711, A61K31/711.5, A61K31/712,
PC A61K31/712.5, A61K33/24, A61K48/00, A61P35/00, A61P43/00, C07H21/04,
PC C12N5/10//
PC (C12N5/10, C12R1:91), C12N15/00, C12N5/00, (C12N5/00, C12R1:91) CC
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FH Key Location/Qualifiers
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Best Local Similarity 61.1%; Pred. No. 1.6e+05;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 CGGAGCGGGAUGCCUU 20
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Db 20 CGGCGCTGGGATCTTT 3
RESULT 20
BD246851/c
LOCUS BD246851 37 bp DNA linear PAT 17-JUL-2003
DEFINITION Use of fluorescent molecular beacons in the detection of methylated

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nucleic acids.
BD246851
VERSION BD246851.1 GI:33056621
KEYWORDS JP 2002535998-A/4.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Kay, P.H.
TITLE Use of fluorescent molecular beacons in the detection of methylated
JOURNAL nucleic acids
COMMENT Patent: JP 2002535998-A 4 29-OCT-2002;
THE UNIVERSITY OF WESTERN AUSTRALIA
OS Preferable target sequence of the glutathione-S-transferase
(p1) gene
PN JP 2002535998-A/4
PD 29-OCT-2002
PF 01-FEB-2000 JP 2000597457
PR 01-FEB-1999 AU PP 8448
PI PETER H KAY
PC C12N15/09, C12Q1/68, G01N33/53, G01N33/566, C12N15/00 CC Use of
fluorescent molecular beacons in the detection of CC
methylated
CC nucleic acids
FH Key Location/Qualifiers
FT source 1..37
FT /organism="Homo sapiens"
FT /mol_type="genomic DNA"
FT /db_xref="taxon:32644"
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Location/Qualifiers
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Best Local Similarity 72.2%; Pred. No. 1.5e+05;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 26 CGGAGGCGCGGAGGCCCTT 9

RESULT 21
AX513936
LOCUS 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 134 from Patent WO02052044.
ACCESSION AX513936
VERSION AX513936.1 GI:23560241
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 134 04-JUL-2002;
Riken (JP)
FEATURES
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1..41
Location/Qualifiers
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Best Local Similarity 60.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACGAGCGCGGAGGCCUU 20
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Db 1 AACGAGCGCGGAGGCCCT 18

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Db 18 ACCRAGCCTGGGGTGCCT 37

RESULT 22
AX519275
LOCUS 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 5473 from Patent WO02052044.
ACCESSION AX519275
VERSION AX519275.1 GI:23569440
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 5473 04-JUL-2002;
Riken (JP)
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
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Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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Db 18 ACCRAGCCTGGGGTGCCT 37

RESULT 23
BD062551
LOCUS 18 bp DNA linear PAT 27-AUG-2002
DEFINITION ICAM-6 materials and methods.
ACCESSION BD062551
VERSION BD062551.1 GI:22608154
KEYWORDS JP 2001506139-A/37.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 18)
AUTHORS Loughney, K., Staunton, D.E. and Vazeau, R.
TITLE ICAM-6 materials and methods
JOURNAL Patent: JP 2001506139-A 37 15-MAY-2001;
ICOS CORP
COMMENT OS Artificial Sequence
PN JP 2001506139-A/37
PD 15-MAY-2001
PF 22-OCT-1998 JP 1999524640
PR 22-OCT-1997 US 08/955661
PI KATE LOUGHNEY, DONALD E STAUNTON, ROSEMARY VAZEAU PC
C12N15/12, C07K14/705, C12N15/11, C07K16/28, C07K16/42 CC Description
of Artificial Sequence: primer
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Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGAGGCGCGGAGGCC 16
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Db 6 GGAGGCGCGGAGT 18

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RESULT 24
AR307817
LOCUS AR307817 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 28 from patent US 6551826.
ACCESSION AR307817
VERSION AR307817.1 GI:31698573
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS Watt,A.T.
TITLE Antisense modulation of raidd expression
JOURNAL Patent: US 6551826-A 28 22-APR-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 84.6%; Pred. No. 2.1e+05;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 6 AGGCGGGGAGGCC 18
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Db 6 AGGCTGGGATGCC 18

RESULT 25
AR217789
LOCUS AR217789 22 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 26 from patent US 6416987.
ACCESSION AR217789
VERSION AR217789.1 GI:23317671
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 22)
AUTHORS Liu-Chen,X., Tong,Y., Bertino,J.R. and Banerjee,D.
TITLE Mutants of thymidylate synthase and uses thereof
JOURNAL Patent: US 6416987-A 26 09-JUL-2002;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 84.6%; Pred. No. 2.1e+05;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 6 AGGCGGGGAGGCC 18
||||:||||:
Db 10 AGGCTGGGATGCC 22

Search completed: May 24, 2005, 10:52:06
Job time : 1842 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 06:20:49 ; Search time 424 Seconds
(without alignments)
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Title: US-10-018-437-2

Perfect score: 20
Sequence: 1 aacggaggcgggaugccu 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	4	AAC86402
C 2	20	100.0	20	4	AAC86403
C 3	18.4	92.0	20	4	AAC86405
C 4	18.2	91.0	29	3	AAC65050
C 5	16.2	81.0	20	3	AAC65051
C 6	15.2	76.0	20	4	AAC86401
C 7	15.2	76.0	20	4	AAC86404
C 8	15.2	76.0	20	9	ADA24238
C 9	15	75.0	19	10	ADF49386
C 10	15	75.0	19	10	ADF49800
C 11	14.8	74.0	29	11	ADM33364
C 12	14.8	74.0	29	11	ADM33363
C 13	14.8	74.0	29	11	ADM33841
C 14	14.8	74.0	29	11	ADM33840
C 15	14.8	74.0	29	13	ADR48971
C 16	14.8	74.0	29	13	ADR48972
C 17	14.4	72.0	17	8	ACD65499
C 18	14.4	72.0	17	8	ACD54170
C 19	14.4	72.0	17	12	ADI87105
C 20	14.4	72.0	17	12	ADI82958

94	12.6	63.0	30	12	AD056882	Ad056882 Human CAR
95	12.6	63.0	31	4	AAI30956	AAI30956 Human sin
C 96	12.6	63.0	34	10	ABZ75557	ABZ75557 Partial b
97	12.6	63.0	36	3	AZ40039	AZ40039 PCR prime
C 98	12.6	63.0	36	3	AZ40038	AZ40038 PCR prime
99	12.6	63.0	36	4	AAC87933	AAC87933 B43 scFv
C 100	12.6	63.0	40	12	ADJ45006	ADJ45006 Plant cDN
C 101	12.6	63.0	41	5	AAI66119	AAI66119 Human amy
C 102	12.6	63.0	42	3	AA58596	AA58596 PCR prime
C 103	12.6	63.0	42	6	ABN89440	ABN89440 Human FC
C 104	12.6	63.0	42	10	AD53742	AD53742 Human IgG
C 105	12.6	63.0	47	3	AAZ67573	AAZ67573 Human map
106	12.6	63.0	50	4	AAI34563	AAI34563 Human SNP
107	12.6	63.0	50	6	ABZ04605	ABZ04605 Human leu
108	12.6	63.0	50	2	AAZ22404	AAZ22404 Human liv
C 109	12.4	62.0	18	3	AAZ91443	AAZ91443 Human Shi
110	12.4	62.0	20	2	AAV85771	AAV85771 LRP5 exon
111	12.4	62.0	20	2	AAV85849	AAV85849 LRP5 SNP
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C 113	12.4	62.0	21	2	AAI95453	AAI95453 Capture o
114	12.4	62.0	21	6	AAK50474	AAK50474 Hepatitis
C 115	12.4	62.0	23	10	AD55589	AD55589 IG57272 H
C 116	12.4	62.0	24	6	AB188490	AB188490 Capture o
117	12.4	62.0	24	6	AB187477	AB187477 Capture o
C 118	12.4	62.0	24	6	AB187476	AB187476 Capture o
119	12.4	62.0	25	9	AB188491	AB188491 Capture o
C 120	12.4	62.0	25	6	ACI64549	ACI64549 Human mic
121	12.4	62.0	25	12	AD040618	AD040618 Human WMP
C 122	12.4	62.0	27	10	ADC68491	ADC68491 Invertase
123	12.4	62.0	28	2	AAQ65320	AAQ65320 PCR prime
124	12.4	62.0	28	2	AAQ86797	AAQ86797 Hepatitis
125	12.4	62.0	29	2	AAV38858	AAV38858 HCV core
C 126	12.4	62.0	29	3	AAA04115	AAA04115 Polymorph
127	12.4	62.0	31	2	AAV06270	AAV06270 Human bia
128	12.4	62.0	34	6	ABL31982	ABL31982 FokI loop
129	12.4	62.0	37	6	AAV39148	AAV39148 Human her
130	12.4	62.0	40	2	AAV85850	AAV85850 LRP5 SNP
131	12.4	62.0	40	2	AAV85772	AAV85772 LRP5 exon
132	12.4	62.0	50	6	ABZ05750	ABZ05750 Human leu
C 133	12.2	61.0	17	6	ABK19187	ABK19187 Human ERG
C 134	12.2	61.0	17	6	ABK17969	ABK17969 Human ERG
135	12.2	61.0	19	2	AAV74858	AAV74858 Porcine r
136	12.2	61.0	19	4	AAV77774	AAV77774 PCR prime
137	12.2	61.0	19	12	ADK43461	ADK43461 Porcine r
138	12.2	61.0	19	13	AD573416	AD573416 Swine ret
C 139	12.2	61.0	20	10	ADB81525	ADB81525 Antisense
C 140	12.2	61.0	21	2	AAZ26708	AAZ26708 Human pol
141	12.2	61.0	21	2	AAZ36758	AAZ36758 PCR prime
142	12.2	61.0	21	4	ABL55916	ABL55916 Human BPI
143	12.2	61.0	21	6	ABX09358	ABX09358 Arteriosc
C 144	12.2	61.0	22	2	AAV76053	AAV76053 Human Nip
145	12.2	61.0	22	12	AD011777	AD011777 Single mu
C 146	12.2	61.0	24	2	AAV09238	AAV09238 Factor XI
C 147	12.2	61.0	24	2	AAV92596	AAV92596 BRC2 can
C 148	12.2	61.0	24	6	AAI53446	AAI53446 Type II t
C 149	12.2	61.0	24	6	AAI53449	AAI53449 Type II t
C 150	12.2	61.0	25	9	ACK17903	ACK17903 Human mic

ALIGNMENTS

RESULT 1
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 ID AAC86402 standard; mRNA; 20 BP.
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 AC AAC86402;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human bcl-2 mRNA nucleotides 2032-2051.
 XX
 KW Human; bcl-xL; bcl-2; apoptosis; cancer; allergic disease;

KW restenosis; fibrosis; psoriasis; ss.
 OS Homo sapiens.
 XX
 FN WO200066724-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-EP003708.
 XX
 PR 30-APR-1999; 99GB-00010119.
 XX
 PA (UYZU-) UNIV ZUERICH.
 XX
 PI Zangemeister-Wittke U, Luedke G, Huesken D;
 XX
 DR WPI; 2001-015981/02.
 XX
 PS Antisense oligonucleotide derivatives directed against human bcl-xL mRNA
 XX and capable of modulating biosynthesis of human bcl-xL proteins, useful
 XX in treatment and diagnosis of hyperproliferative diseases.
 XX
 PS Disclosure; Page 5; 38pp; English.
 XX
 CC The present invention provides antisense nucleotides which hybridize to
 CC the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins
 CC are involved in apoptosis, and the antisense strands can be used to
 CC inhibit them and possibly lead to cell death. The nucleic acids of the
 CC invention can be used in the treatment of cancer, particularly
 CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,
 CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain
 CC types of allergic disease
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 SQ Sequence 20 BP; 4 A; 4 C; 8 G; 0 T; 4 U; 0 Other;
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 Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 AACGAGGCGUGGAGCCUU 20
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 XX
 AC AAC86403;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human bcl-xL and bcl-2 mRNA antisense sequence #1.
 XX
 KW Human; bcl-xL; bcl-2; apoptosis; antisense; cancer; allergic disease;
 KW restenosis; fibrosis; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200066724-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-EP003708.
 XX
 PR 30-APR-1999; 99GB-00010119.
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 PA (UYZU-) UNIV ZUERICH.
 XX
 PI Zangemeister-Wittke U, Luedke G, Huesken D;
 XX
 DR WPI; 2001-015981/02.
 XX

PT Antisense oligonucleotide derivatives directed against human bcl-xL mRNA
 PT and capable of modulating biosynthesis of human bcl-xL proteins, useful
 PT in treatment and diagnosis of hyperproliferative diseases.

PS Claim 6; Page 29; 38pp; English.

XX The present invention provides antisense nucleotides which hybridize to
 CC the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins
 CC are involved in apoptosis, and the antisense strands can be used to
 CC inhibit them and possibly lead to cell death. The nucleic acids of the
 CC invention can be used in the treatment of cancer, particularly
 CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,
 CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain
 CC types of allergic disease

SQ Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;

Best Local Similarity 80.0%; Pred. No. 10;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGATGCTTT 20

Db 20 AACGGAGGCTGGGATGCTTT 1

RESULT 3

AAC86405/c

ID AAC86405 standard; RNA; 20 BP.

XX AC AAC86405;

DT 28-FEB-2001 (first entry)

DE Human bcl-xL and bcl-2 mRNA antisense sequence #3.

XX Human; bcl-xL; bcl-2; apoptosis; antisense; cancer; allergic disease;
 KW restenosis; fibrosis; psoriasis; ss.

OS Homo sapiens.

XX WO200066724-A2.

XX 09-NOV-2000.

PF 26-APR-2000; 2000WO-EP003708.

XX 30-APR-1999; 99GB-00010119.

XX (UYZU-) UNIV ZUERICH.

XX Zangemeister-Wittke U, Luedke G, Huesken D;

XX WPI; 2001-015981/02.

PT Antisense oligonucleotide derivatives directed against human bcl-xL mRNA
 PT and capable of modulating biosynthesis of human bcl-xL proteins, useful
 PT in treatment and diagnosis of hyperproliferative diseases.

PS Claim 6; Page 29; 38pp; English.

XX The present invention provides antisense nucleotides which hybridize to
 CC the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins
 CC are involved in apoptosis, and the antisense strands can be used to
 CC inhibit them and possibly lead to cell death. The nucleic acids of the
 CC invention can be used in the treatment of cancer, particularly
 CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,
 CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain
 CC types of allergic disease

SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 4; Length 20;

Best Local Similarity 75.0%; Pred. No. 57;
 Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGATGCTTT 20

Db 20 AACGGAGGCTGGGATGCTTT 1

RESULT 4

AAC65050/c

ID AAC65050 standard; DNA; 29 BP.

AC AAC65050;

DT 12-FEB-2001 (first entry)

DE Human bcl genes antisense sequence #3.

XX Antisense oligonucleotide; RNA molecule cleavage; immune activation; bcl;
 KW protein kinase C; PKC; PCR primer; ss.

OS Homo sapiens.

XX WO200061810-A1.

XX 19-OCT-2000.

XX 07-APR-2000; 2000WO-US009293.

XX 08-APR-1999; 99US-0128377P.

XX (OASI-) OASIS BIOSCIENCES INC.

XX Brown BD, Riley TA;

XX WPI; 2000-679502/66.

PT Antisense oligonucleotides containing degenerate and/or universal bases,
 PT and modified backbone linkages is useful to target therapeutic genes,
 PT preferably anti-apoptosis or chemoresistance genes.

XX Example 5; Fig 1; 32pp; English.

XX The present invention is concerned with antisense oligonucleotides
 CC containing a number of degenerate bases and with a modified backbone
 CC which can be used to direct cleavage of target RNA molecules. The use of
 CC degenerate bases reduces the risk of immune activation following
 CC injection into animals, which causes deleterious side effects associated
 CC with many therapeutic antisense oligonucleotides. Sequences AAC65029-
 CC C65077 are antisense oligonucleotides and PCR primers used in assays to
 CC demonstrate the effects of the sequences of the invention

SQ Sequence 29 BP; 6 A; 12 C; 3 G; 4 T; 0 U; 4 Other;

Query Match 91.0%; Score 18.2; DB 3; Length 29;

Best Local Similarity 65.0%; Pred. No. 72;
 Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGATGCTTT 20

Db 25 AACGGAGGCTGGGATGCTTT 6

RESULT 5

AAC65051/c

ID AAC65051 standard; DNA; 20 BP.

XX AC AAC65051;

DT 12-FEB-2001 (first entry)

XX Human bcl genes antisense sequence #4.

KW Antisense oligonucleotide; RNA molecule cleavage; immune activation; bcl;
KW protein kinase C; PKC; PCR primer; ss.
XX Homo sapiens.
OS

XX WO200061810-A1.
XX
XX 19-OCT-2000.
XX

XX 07-APR-2000; 2000WO-US009293.
XX
XX 08-APR-1999; 99US-0128377P.
XX

XX (OASI-) OASIS BIOSCIENCES INC.
XX
XX Brown BD, Riley TA;
XX

XX WPI; 2000-679502/66.
XX
XX Antisense oligonucleotides containing degenerate and/or universal bases,
XX and modified backbone linkages is useful to target therapeutic genes,
XX preferably anti-apoptosis or chemoresistance genes.
XX

XX Example 5; Fig 1; 32pp; English.
XX
XX The present invention is concerned with antisense oligonucleotides
XX containing a number of degenerate bases and with a modified backbone
XX which can be used to direct cleavage of target RNA molecules. The use of
XX degenerate bases reduces the risk of immune activation following
XX injection into animals, which causes deleterious side effects associated
XX with many therapeutic antisense oligonucleotides. Sequences AAC65029-
XX C65077 are antisense oligonucleotides and PCR primers used in assays to
XX demonstrate the effects of the sequences of the invention
XX

XX Sequence 20 BP; 5 A; 8 C; 3 G; 1 T; 0 U; 3 Other;
XX
XX Query Match 81.0%; Score 16.2; DB 3; Length 20;
XX Best Local Similarity 61.1%; Pred. No. 6.1e+02;
XX Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGGAGCGCUGGAGCCUU 20
DB 20 CGGNGGCTGGGATRCYTT 3
RESULT 6
AAC86401
ID AAC86401 standard; mRNA; 20 BP.
XX
XX AAC86401;
XX
XX 28-FEB-2001 (first entry)
XX
XX Human bcl-xL mRNA nucleotides 687-706.
XX

XX Human; bcl-xL; bcl-2; apoptosis; antisense; cancer; allergic disease;
XX restenosis; fibrosis; psoriasis; ss.
XX Homo sapiens.
XX WO200066724-A2.
XX
XX 09-NOV-2000.
XX
XX 26-APR-2000; 2000WO-EP003708.
XX
XX 30-APR-1999; 99GB-00010119.
XX
XX (UYZU-) UNIV ZUERICH.
XX
XX Zangemeister-Wittke U, Luedke G, Huesken D;
XX WPI; 2001-015981/02.
XX

XX

PT Antisense oligonucleotide derivatives directed against human bcl-xL mRNA
PT and capable of modulating biosynthesis of human bcl-xL proteins, useful
PT in treatment and diagnosis of hyperproliferative diseases.

XX Disclosure; Page 4; 38pp; English.
XX

XX The present invention provides antisense nucleotides which hybridise to
XX the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins
XX are involved in apoptosis, and the antisense strands can be used to
XX inhibit them and possibly lead to cell death. The nucleic acids of the
XX invention can be used in the treatment of cancer, particularly
XX colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,
XX neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain
XX types of allergic disease
XX

SQ Sequence 20 BP; 4 A; 4 C; 7 G; 0 T; 5 U; 0 Other;
Query Match 76.0%; Score 15.2; DB 4; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AACGAGCGCUGGAGCCUU 20
DB 1 AACGCGCGCUGGAGUACUU 20
RESULT 7
AAC86404/c
ID AAC86404 standard; RNA; 20 BP.
XX
XX AAC86404;
XX
XX 28-FEB-2001 (first entry)
XX
XX Human bcl-xL and bcl-2 mRNA antisense sequence #2.
XX
XX Human; bcl-xL; bcl-2; apoptosis; antisense; cancer; allergic disease;
XX restenosis; fibrosis; psoriasis; ss.
XX
XX Homo sapiens.
XX
XX WO200066724-A2.
XX
XX 09-NOV-2000.
XX
XX 26-APR-2000; 2000WO-EP003708.
XX
XX 30-APR-1999; 99GB-00010119.
XX
XX (UYZU-) UNIV ZUERICH.
XX
XX Zangemeister-Wittke U, Luedke G, Huesken D;
XX WPI; 2001-015981/02.
XX

PT Antisense oligonucleotide derivatives directed against human bcl-xL mRNA
PT and capable of modulating biosynthesis of human bcl-xL proteins, useful
PT in treatment and diagnosis of hyperproliferative diseases.

XX Disclosure; Page 4; 38pp; English.
XX

XX The present invention provides antisense nucleotides which hybridise to
XX the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins
XX are involved in apoptosis, and the antisense strands can be used to
XX inhibit them and possibly lead to cell death. The nucleic acids of the
XX invention can be used in the treatment of cancer, particularly
XX colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,
XX neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain
XX types of allergic disease
XX

SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 81.0%; Score 16.2; DB 3; Length 20;
Best Local Similarity 61.1%; Pred. No. 6.1e+02;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGGAGCGCUGGAGCCUU 20
DB 20 CGGNGGCTGGGATRCYTT 3
RESULT 6
AAC86401
ID AAC86401 standard; mRNA; 20 BP.
XX
XX AAC86401;
XX
XX 28-FEB-2001 (first entry)
XX
XX Human bcl-xL mRNA nucleotides 687-706.
XX

XX Human; bcl-xL; bcl-2; apoptosis; antisense; cancer; allergic disease;
XX restenosis; fibrosis; psoriasis; ss.
XX Homo sapiens.
XX WO200066724-A2.
XX
XX 09-NOV-2000.
XX
XX 26-APR-2000; 2000WO-EP003708.
XX
XX 30-APR-1999; 99GB-00010119.
XX
XX (UYZU-) UNIV ZUERICH.
XX
XX Zangemeister-Wittke U, Luedke G, Huesken D;
XX WPI; 2001-015981/02.
XX

Query Match 76.0%; Score 15.2; DB 4; Length 20;
 Best Local Similarity 65.0%; Pred. No. 1.8e+03;
 Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 AACGGAGGCGGGAUGCCUU 20
 ||||| ||||| ||||| : :
 DB 20 AACGGCGGCTGGGATACCTT 1

RESULT 8
 ADA24238/c
 ID ADA24238 standard; DNA; 20 BP.
 XX
 AC ADA24238;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human bcl-xl antisense oligonucleotide MB-003 SEQ ID NO:21.
 XX
 KW therapeutic oligonucleotide; double-stranded RNA; dsRNA; mobile protein;
 KW cytosolic; immunosuppressive; virucide; anti-HIV; antibacterial;
 KW cardiant; hyperproliferation; cancer; haematological; metastatic;
 KW autoimmune disease; infection; endocrine; neural; cardiovascular;
 KW pulmonary; reproductive system disorder; endocytosis; metabolic process;
 KW murine; intracellular adhesion molecule 1; ICAM-1;
 KW antisense oligonucleotide; phosphorothioate; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone"
 XX
 FN WO2003069306-A2.
 XX
 PD 21-AUG-2003.
 XX
 PF 13-FEB-2003; 2003WO-US004323.
 XX
 PR 13-FEB-2002; 2002US-0356053P.
 XX
 PA (MEDB-) MEDBRIDGE INC.
 XX
 PI Xie D;
 XX
 DR WPI; 2003-646491/61.
 XX
 PT Treating diseases with oligonucleotides or interfering RNA, useful e.g.
 PT for cancer or autoimmune diseases, covalently coupled to mobile proteins,
 PT in vivo or in vitro.
 XX
 PS Claim 128; Page 12; 42pp; English.
 XX
 CC The present invention describes a method for treating a disease by
 CC administering; (a) a therapeutic oligonucleotide (TON) or double-stranded
 CC RNA (dsRNA) that includes a reactive group (RG) that can react with a
 CC mobile protein (MP) to form a covalent conjugate of TON/dsRNA and MP; or
 CC (b) TON or dsRNA already conjugated to MP through a covalent bond. Also
 CC described: (1) TON of 15-30 bases that includes (i) a part that binds to
 CC target RNA or DNA and (ii) RG; (2) TON of 15-30 bases that includes a
 CC part that binds to target RNA or DNA and is conjugated to MP through a
 CC covalent link; (3) dsRNA that includes RG; and (4) dsRNA that is
 CC conjugated to MP through a covalent link. TON have cytosolic,
 CC immunosuppressive, virucide, anti-HIV, antibacterial and cardiant
 CC activities. The method is used to treat, or prevent, hyperproliferation
 CC (particularly cancers, solid or haematological, including prevention of
 CC metastatic spread); autoimmune diseases; viral or bacterial infections;
 CC endocrine, neural, cardiovascular, pulmonary or reproductive system
 CC disorders. Also where TON or dsRNA are labelled, they can be used for
 CC diagnosis and monitoring of therapy. When linked to a mobile protein,

CC TON/dsRNA have better cell entry (via endocytosis or other parts of the
 CC mobile protein metabolic process) and longer therapeutic life, increased
 CC from hours to weeks (the result of increased resistance to nuclease),
 CC without loss of affinity for the target. In many cases immune response to
 CC TON/dsRNA is also reduced, as is non-specific binding to endogenous
 CC proteins. The present sequence represents a human bcl-xl antisense
 CC oligonucleotide, which is a specifically claimed TON from the present
 CC invention.
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 76.0%; Score 15.2; DB 9; Length 20;
 Best Local Similarity 65.0%; Pred. No. 1.8e+03;
 Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 AACGGAGGCGGGAUGCCUU 20
 ||||| ||||| ||||| : :
 DB 20 AACGGCGGCTGGGATACCTT 1

RESULT 9
 ADF49386
 ID ADF49386 standard; RNA; 19 BP.
 XX
 AC ADF49386;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human BCL2 siRNA lower sequence SEQ ID NO:114.
 XX
 KW ss; siRNA; human; BCL2; short interfering nucleic acid; RNA interference;
 KW cytosolic; immunosuppressive; virucide; anti-HIV; cancer;
 KW autoimmune disease; viral infection; HIV.
 XX
 OS Homo sapiens.
 XX
 FN WO2003070969-A2.
 XX
 PD 28-AUG-2003.
 XX
 PF 18-FEB-2003; 2003WO-US004908.
 XX
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 18-JUL-2002; 2002US-0396905P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J, Beigelman L;
 XX
 DR WPI; 2003-712622/67.
 XX
 PT New short interfering nucleic acid, useful e.g. for treatment and
 PT diagnosis of cancer or autoimmune disease, downregulates expression of
 PT the BCL2 gene.
 XX
 PS Example 3; SEQ ID NO 114; 148pp; English.
 XX
 CC The invention relates to a novel short interfering nucleic acid (siRNA)
 CC that downregulates expression of the BCL2 gene by RNA interference. A
 CC siRNA of the invention has cytosolic, immunosuppressive, virucide, and
 CC anti-HIV activity. The siRNA are useful for modulation (inhibition) of
 CC expression or activity of BCL2 by RNA interference. siRNA are used to
 CC modulate expression of BCL2 genes, in cells, tissue explants or
 CC organisms, e.g. for treating cancer, autoimmune diseases and viral
 CC infections (including by HIV) but also for drug screening, diagnosis,
 CC target identification and validation, genetic engineering,
 CC pharmacogenomics, studying gene function and gene mapping (e.g. of single

CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
CC represent siNA of the invention.
XX
SQ Sequence 19 BP; 2 A; 3 C; 8 G; 0 T; 6 U; 0 Other;
Query Match 75.0%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 AGGCGGGAGGCCUU 20
DB 1 AGGCGGGAGGCCUU 15
|||||
RESULT 10
ADF49800/C
ID ADF49800 standard; RNA; 19 BP.
XX
AC ADF49800;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human BCL2 siNA lower sequence SEQ ID NO:528.
XX
KW ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;
KW cytotatic; immunosuppressive; virucide; anti-HIV; cancer;
KW autoimmune disease; viral infection; HIV.
XX
OS Homo sapiens.
XX
PN WO2003070969-A2.
XX
PD 28-AUG-2003.
XX
PF 18-FEB-2003; 2003WO-US004908.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 18-JUL-2002; 2002US-0396905P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman J;
XX
DR WPI; 2003-712622/67.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer or autoimmune disease, downregulates expression of
PT the BCL2 gene.
XX
PS Example 3; SEQ ID NO 528; 148pp; English.
XX
CC The invention relates to a novel short interfering nucleic acid (siNA)
CC that downregulates expression of the BCL2 gene by RNA interference. A
CC siNA of the invention has cytotatic, immunosuppressive, virucide, and
CC anti-HIV activity. The siNA are useful for modulation (inhibition) of
CC expression or activity of BCL2 by RNA interference. siNA are used to
CC modulate expression of BCL2 genes, in cells, tissue explants or
CC organisms, e.g. for treating cancer, autoimmune diseases and viral
CC infections (including by HIV) but also for drug screening, diagnosis,
CC target identification and validation, genetic engineering,
CC pharmacogenomics, studying gene function and gene mapping (e.g. of single
CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
CC represent siNA of the invention.
XX
SQ Sequence 19 BP; 6 A; 8 C; 3 G; 0 T; 2 U; 0 Other;
Query Match 75.0%; Score 15; DB 10; Length 19;

Best Local Similarity 73.3%; Pred. No. 2.2e+03;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 6 AGGCGGGAGGCCUU 20
DB 19 AGGCTGGGATGCCTT 5
|||||
RESULT 11
ADM33364/C
ID ADM33364 standard; DNA; 29 BP.
XX
AC ADM33364;
XX
DT 03-JUN-2004 (first entry)
XX
DE Immunoglobulin G2 (IgG2) fragment of crystallisation primer seqid 6.
XX
KW cytotatic; immunostimulant; antianaemic; anti-HIV; protein therapy;
KW human; granulocyte colony-stimulating factor; GCSF; GCSF-L-vFc;
KW immunoglobulin G; IgG; fragment of crystallisation; immune disorder;
KW haematopoietic disorder; cancer; chemotherapy; leukaemia; anaemia; AIDS;
KW bone marrow transplantation; chronic neutropenia;
KW reverse transcriptase PCR; RT-PCR; primer; ss; immunoglobulin G2; IgG2;
KW fragment of crystallisation; Fc; Fcgamma2; mutagenesis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2003082679-A1.
XX
PD 01-MAY-2003.
XX
PF 01-OCT-2001; 2001US-00968362.
XX
PR 01-OCT-2001; 2001US-00968362.
XX
PA (SUNL/) SUN L K.
PA (SUNB/) SUN B N C.
PA (SUNC/) SUN C R Y.
XX
PI Sun LK, Sun BNC, Sun CRY;
XX
DR WPI; 2003-585400/55.
XX
PT New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-
PT vFc fusion protein for treating immune or hematopoietic system disorders
PT comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin G
PT Fc variant.
XX
PS Disclosure; SEQ ID NO 6; 15pp; English.
XX
CC The invention describes a recombinant human granulocyte colony-
CC stimulating factor (hG-CSF)-L-vFc fusion protein comprising hG-CSF, a
CC peptide linker, and a human immunoglobulin G (IgG) Fc variant. Also
CC described are: a CHO-derived cell line producing the above hG-CSF-L-vFc
CC fusion protein in its growth medium in excess of 10 μ g/ml per million
CC cells in a 24-hour period; and making the recombinant fusion protein
CC cited above, comprising generating a CHO-derived cell line cited above,
CC growing the cell line under conditions the recombinant fusion protein is
CC expressed in its growth medium, and purifying the expressed protein. The
CC recombinant fusion protein is useful in treating a variety of conditions
CC associated with an impaired immune or haematopoietic system, including
CC cancer chemotherapy, leukaemias, anaemias, AIDS, bone marrow
CC transplantation, and chronic neutropenias. This sequence represents a
CC primer used in the creation of DNA encoding a human immunoglobulin G2
CC (IgG2) fragment of crystallisation gamma 2 (Fcgamma2) Pro331Ser variant.
XX
SQ Sequence 29 BP; 9 A; 12 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 74.0%; Score 14.8; DB 11; Length 29;
Best Local Similarity 77.8%; Pred. No. 2.8e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCGUGGAGCCU 19
 | |||||:|||||:|
 Db 18 ATGGAGGCTGGAGGCGCT 1

RESULT 12
 ADM33363
 ID ADM33363 standard; DNA; 29 BP.
 XX AC ADM33363;
 XX DT 03-JUN-2004 (first entry)
 XX DE Immunoglobulin G2 (IgG2) fragment of crystallisation primer seqid 5.
 XX KW cytostatic; immunostimulant; antianaemic; anti-HIV; protein therapy;
 KW human; granulocyte colony-stimulating factor; GCSF; GCSF-L-vFc;
 KW immunoglobulin G; IgG; fragment of crystallisation; immune disorder;
 KW haematopoietic disorder; cancer; chemotherapy; leukaemia; anaemia; AIDS;
 KW bone marrow transplantation; chronic neutropenia;
 KW reverse transcriptase PCR; RT-PCR; primer; ss; immunoglobulin G2; IgG2;
 KW fragment of crystallisation; Fc; Fcgamma2; mutagenesis.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN US2003082679-A1.
 XX PD 01-MAY-2003.
 XX PF 01-OCT-2001; 2001US-00968362.
 XX PR 01-OCT-2001; 2001US-00968362.
 XX PA (SUNL/) SUN L K.
 XX PA (SUNB/) SUN B N C.
 XX PA (SUNC/) SUN C R Y.
 XX PI Sun LK, Sun BNC, Sun CRY;
 XX WPI; 2003-585400/55.
 XX PS New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-
 XX vFc fusion protein for treating immune or hematopoietic system disorders
 XX comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin G
 XX Fc variant.
 XX PS Disclosure; SEQ ID NO 5; 15pp; English.
 XX CC The invention describes a recombinant human granulocyte colony-
 XX stimulating factor (hG-CSF)-L-vFc fusion protein comprising hG-CSF, a
 XX peptide linker, and a human immunoglobulin G (IgG) Fc variant. Also
 XX described are: a CHO-derived cell line producing the above hG-CSF-L-vFc
 XX fusion protein in its growth medium in excess of 10 μ g/ml per million
 XX cells in a 24-hour period; and making the recombinant fusion protein
 XX cited above, comprising generating a CHO-derived cell line cited above,
 XX growing the cell line under conditions the recombinant fusion protein is
 XX expressed in its growth medium, and purifying the expressed protein. The
 XX recombinant fusion protein is useful in treating a variety of conditions
 XX associated with an impaired immune or hematopoietic system, including
 XX cancer chemotherapy, leukemias, anemias, AIDS, bone marrow
 XX transplantation, and chronic neutropenias. This sequence represents a
 XX primer used in the creation of DNA encoding a human immunoglobulin G2
 XX (IgG2) fragment of crystallisation gamma 2 (Fcgamma2) Pro331Ser variant.
 XX Sequence 29 BP; 3 A; 5 C; 12 G; 9 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 11; Length 29;
 Best Local Similarity 77.8%; Pred. No. 2.8e+03;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCGUGGAGCCU 19
 | |||||:|||||:|

Db 12 ATGGAGGCTGGAGGCGCT 29

RESULT 13
 ADM33841/C
 ID ADM33841 standard; DNA; 29 BP.
 XX AC ADM33841;
 XX DT 03-JUN-2004 (first entry)
 XX DE Human IgG2 Fc mutagenic PCR primer #2.
 XX KW Human; erythropoietin; ss; PCR; primer; EPO; immunoglobulin; IgG;
 KW fragment crystallisation region; Fc; chronic anaemia; renal disease;
 KW cancer chemotherapy; rheumatoid arthritis; AIDS;
 KW myelodysplastic syndrome; (HuEPO)-L-vFc.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN US2003082749-A1.
 XX PD 01-MAY-2003.
 XX PF 17-AUG-2001; 2001US-00932812.
 XX PR 17-AUG-2001; 2001US-00932812.
 XX PA (SUNL/) SUN L K.
 XX PA (SUNB/) SUN B N C.
 XX PA (SUNC/) SUN C R Y.
 XX PI Sun LK, Sun BNC, Sun CRY;
 XX WPI; 2003-616080/58.
 XX PS New recombinant human erythropoietin-L-vFc fusion proteins, useful for
 XX treating patients with chronic anemia caused by renal failure, cancer
 XX chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV
 XX infection.
 XX PS Disclosure; SEQ ID NO 6; 14pp; English.
 XX CC The invention relates to a recombinant human erythropoietin (HuEPO)-L-vFc
 XX fusion protein comprising HuEPO, a peptide linker, and a human
 XX immunoglobulin G Fc (fragment crystallisation region) variant. Also
 XX included is a carbohydrate-derived cell line producing the human
 XX erythropoietin-L-vFc fusion protein cited above in its growth medium in
 XX excess of 10 microgramme per million cells in a 24-hour period. The HuEPO
 XX -L-vFc fusion protein exhibits an enhanced in vitro biological activity
 XX of at least 2-fold relative to that of recombinant HuEPO on a molar
 XX basis. The flexible peptide linker containing about 20 or fewer amino
 XX acids is present between HuEPO and the human IgG Fc variant. The IgG Fc
 XX contains amino acid mutations to attenuate effector functions. The human
 XX IgG Fc variant comprises a hinge, CH2 and CH3 domains of human IgG2 with
 XX Pro331Ser mutation, human IgG4 with Ser228Pro and Leu235Ala mutations, or
 XX human IgG1 with Leu234Val, Leu235Ala and Pro331Ser mutations. The
 XX recombinant human erythropoietin-L-vFc fusion proteins are useful for
 XX treating patients with chronic anaemia caused by renal failure, cancer
 XX chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV
 XX infection, or myelodysplastic syndrome. The increased activity and
 XX prolonged presence of the human erythropoietin-L-vFc fusion protein in
 XX the serum, as compared to prior art, leads to lower dosages and less
 XX frequent injections. Less fluctuations of the drug in serum
 XX concentrations means improved safety and tolerability, and less frequent
 XX injections result in better patient compliance and quality of life. The
 XX present sequence is a mutagenic PCR primer used to create the IgG2 Fc
 XX Pro331Ser cDNA for use in the fusion proteins of the invention.
 XX Sequence 29 BP; 9 A; 12 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 11; Length 29;
Best Local Similarity 77.8%; Pred. No. 2.8e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGCGCGGGAUGCCU 19
| | | | | : | | | | | :
Db 18 ATGGAGGCTGGGAGGCCT 1

RESULT 14
ADM33840
ID ADM33840 standard; DNA; 29 BP.
XX AC
XX ADM33840;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human IgG2 Fc mutagenic PCR primer #1.
XX
KW Human; erythropoietin; ss; PCR; primer; EPO; immunoglobulin; IgG;
KW fragment crystallisation region; Fc; chronic anaemia; renal disease;
KW cancer chemotherapy; rheumatoid arthritis; AIDS;
KW myelodysplastic syndrome; (HuEPO)-L-vFc.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX US2003082749-A1.
XX
XX 01-MAY-2003.
XX
XX 17-AUG-2001; 2001US-00932812.
XX
XX 17-AUG-2001; 2001US-00932812.
XX
XX (SUNL/) SUN L K.
XX (SUNB/) SUN B N C.
XX (SUNC/) SUN C R Y.
XX
XX Sun LK, Sun BNC, Sun CRY;
XX WPI; 2003-616080/58.
XX
XX New recombinant human erythropoietin-L-vFc fusion proteins, useful for
XX treating patients with chronic anemia caused by renal failure, cancer
XX chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV
XX infection.
XX
XX Disclosure; SEQ ID NO 5; 14pp; English.

XX The invention relates to a recombinant human erythropoietin (HuEPO)-L-vFc
XX fusion protein comprising HuEPO, a peptide linker, and a human
XX immunoglobulin G Fc (fragment crystallisation region) variant. Also
XX included is a carbohydrate-derived cell line producing the human
XX erythropoietin-L-vFc fusion protein cited above in its growth medium in
XX excess of 10 microgramme per million cells in a 24-hour period. The HuEPO
XX -L-vFc fusion protein exhibits an enhanced in vitro biological activity
XX of at least 2-fold relative to that of recombinant HuEPO on a molar
XX basis. The flexible peptide linker containing about 20 or fewer amino
XX acids is present between HuEPO and the human IgG Fc variant. The IgG Fc
XX contains amino acid mutations to attenuate effector functions. The human
XX IgG Fc variant comprises a hinge, CH2 and CH3 domains of human IgG2 with
XX Pro331Ser mutation, human IgG4 with Ser228Pro and Leu235Ala mutations, or
XX human IgG1 with Leu234Val, Leu235Ala and Pro331Ser mutations. The
XX recombinant human erythropoietin-L-vFc fusion proteins are useful for
XX treating patients with chronic anaemia caused by renal failure, cancer
XX chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV
XX infection, or myelodysplastic syndrome. The increased activity and
XX prolonged presence of the human erythropoietin-L-vFc fusion protein in
XX the serum, as compared to prior art, leads to lower dosages and less
XX frequent injections. Less fluctuations of the drug in serum
XX concentrations means improved safety and tolerability, and less frequent
XX injections result in better patient compliance and quality of life. The

CC present sequence is a mutagenic PCR primer used to create the IgG2 Fc
CC Pro331Ser cDNA for use in the fusion proteins of the invention.
XX
XX Sequence 29 BP; 3 A; 5 C; 12 G; 7 T; 0 U; 0 Other;
SQ

Query Match 74.0%; Score 14.8; DB 11; Length 29;
Best Local Similarity 77.8%; Pred. No. 2.8e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGCGCGGGAUGCCU 19
| | | | | : | | | | | :
Db 12 ATGGAGGCTGGGAGGCCT 29

RESULT 15
ADR48971
ID ADR48971 standard; DNA; 29 BP.
XX AC
XX ADR48971;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human IgG2 Fc region PCR primer #3.
XX
KW antianemic; nephrotropic; ss; PCR; primer; human; HuEPO-L-vFc;
KW erythropoietin; EPO; anaemia; renal disease; cancer chemotherapy;
KW rheumatoid arthritis; AZT treatment; HIV infection;
KW myelodysplastic syndrome; renal failure.
XX
XX Homo sapiens.
XX
XX US2004175824-A1.
XX
XX 09-SEP-2004.
XX
XX 21-JAN-2004; 2004US-00761593.
XX
XX 17-AUG-2001; 2001US-00932812.
XX
XX (SUNL/) SUN L K.
XX (SUNB/) SUN B N C.
XX (SUNC/) SUN C R Y.
XX
XX Sun LK, Sun BNC, Sun CRY;
XX WPI; 2004-634851/61.
XX
XX New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
XX (HuEPO), a peptide linker, and a human IgG Fc variant, useful for
XX treating chronic anemia due to renal diseases, cancer chemotherapy, or
XX rheumatoid arthritis.
XX
XX Disclosure; SEQ ID NO 5; 31pp; English.

XX A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
XX (HuEPO), a peptide linker, and a human IgG Fc variant, is new.
XX INDEPENDENT CLAIMS are also included for the following: a chinese hamster
XX ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in
XX its growth medium in excess of 10 μ micro; 9 per million cells in a 24 hour
XX period; and a method for making a recombinant fusion protein comprising
XX HuEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred
XX protein: The peptide linker containing 20 or fewer amino acids is present
XX between HuEPO and the human IgG Fc variant, and comprises two or more
XX amino acids selected from glycine, serine, alanine, and threonine. The
XX human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human
XX IgG2 with Pro331Ser mutation comprising 436 amino acids (SEQ ID NO. 18).
XX It also comprises a hinge, CH2, and CH3 domains of human IgG4 with
XX Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.
XX 20). It further comprises a hinge, CH2, and CH3 domains of human IgG1
XX with Leu234Val, Leu235Ala, and Pro331Ser mutations comprising 435 amino
XX acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro
XX biological activity similar to or higher than that of HuEPO on a molar
XX basis. Preferred CHO-Derived Cell Line: The CHO-derived cell line

producing the HuEPO-L-vFc fusion protein in its growth medium in excess of 30 μ mol/g per million cells in a 24 hour period. The human Igg Fc variant comprises a hinge, CH2, CH3 domains of human Igg selected from IgB1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, the Igg Fc contains amino acid mutations to attenuate effector functions, a flexible peptide linker containing 20 or fewer amino acids is present between HuEPO and human Igg Fc variant, and the HuEPO-L-vFc fusion protein exhibits in vitro biological activity similar to or higher than that of rHuEPO on a molar basis. Preferred Method: Making a recombinant fusion protein comprising HuEPO, a flexible peptide linker, and a human Igg Fc variant comprises: generating a CHO-derived cell line; growing the cell line where the recombinant protein is expressed in its growth medium in excess of 10 μ mol/g per million cells in a 24 hour period; and purifying the expressed protein from (b), where the recombinant fusion protein exhibits in vitro biological activity similar to or higher than that of rHuEPO on a molar basis. Antianemic; Nephrotropic. No biological data given. None given. Administration can be through subcutaneous or intravenous route. No dosage given. The recombinant HuEPO-L-vFc fusion protein is useful for treating patients with chronic anemia due to renal diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for HIV infection, or myelodysplastic syndrome. It is also useful in the treatment of renal failure. A fusion protein was assembled from several DNA segments. To obtain the gene encoding the leader peptide and mature protein of human erythropoietin (EPO), cDNA library of human fetal liver or kidney was used as the template in polymerase chain reaction (PCR). For the convenience of cloning, SEQ ID NO. 1 which incorporates a restriction enzyme cleavage site is used as the 5' oligonucleotide primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon and incorporates a BamHI site. The resulting DNA fragments of approximately 600 bp were inserted into a holding vector such as pUC19 at the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the human EPO gene was confirmed by DNA sequencing.

Sequence 29 BP; 3 A; 5 C; 12 G; 9 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 13; Length 29;

Best Local Similarity 77.8%; Pred. No. 2.8e+03;

Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCGGGAGGCCU 19

Db 12 ATGGAGGCTGGGAGGCCT 29

RESULT 16

ADR48972/c

ID ADR48972 standard; DNA; 29 BP.

AC ADR48972;

XX ADR48972;

DT 02-DEC-2004 (first entry)

DE Human IgG2 Fc region PCR primer #4.

XX antianemic; nephrotropic; ss; PCR; primer; human; HuEPO-L-vFc;

KW erythropoietin; EPO; anaemia; renal disease; cancer chemotherapy;

KW rheumatoid arthritis; AZT treatment; HIV infection;

KW myelodysplastic syndrome; renal failure.

XX Homo sapiens.

OS US2004175824-A1.

PN 09-SEP-2004.

PD 21-JAN-2004; 2004US-00761593.

XX 17-AUG-2001; 2001US-00932812.

XX (SUNL/) SUN L K.

FA (SUNB/) SUN B N C.

PA (SUNC/) SUN C R Y.

XX

PI Sun LK, Sun BNC, Sun CRY;

XX WPI; 2004-634851/61.

XX New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin

PT (HuEPO), a peptide linker, and a human Igg Fc variant, useful for

PT treating chronic anemia due to renal diseases, cancer chemotherapy, or

XX rheumatoid arthritis.

XX Disclosure; SEQ ID NO 6; 31pp; English.

XX A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin

CC (HuEPO), a peptide linker, and a human Igg Fc variant, is new.

CC INDEPENDENT CLAIMS are also included for the following: a chinese hamster

CC ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in

CC its growth medium in excess of 10 μ mol/g per million cells in a 24 hour

CC period; and a method for making a recombinant fusion protein comprising

CC HuEPO, a flexible peptide linker, and a human Igg Fc variant. Preferred

CC Protein: The peptide linker containing 20 or fewer amino acids is present

CC between HuEPO and the human Igg Fc variant, and comprises two or more

CC amino acids selected from glycine, serine, alanine, and threonine. The

CC human Igg Fc variant comprises a hinge, CH2, and CH3 domains of human

CC IgG2 with Pro331Ser mutation comprising 436 amino acids (SEQ ID NO. 18).

CC It also comprises a hinge, CH2, and CH3 domains of human IgG4 with

CC Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.

CC 20). It further comprises a hinge, CH2, and CH3 domains of human IgB1

CC with Leu234Val, Leu235Ala, and Pro331Ser mutations comprising 435 amino

CC acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro

CC biological activity similar to or higher than that of rHuEPO on a molar

CC basis. Preferred CHO-Derived Cell Line: The CHO-derived cell line

CC producing the HuEPO-L-vFc fusion protein in its growth medium in excess

CC of 30 μ mol/g per million cells in a 24 hour period. The human Igg Fc

CC variant comprises a hinge, CH2, CH3 domains of human Igg selected from

CC IgB1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20,

CC the Igg Fc contains amino acid mutations to attenuate effector functions,

CC a flexible peptide linker containing 20 or fewer amino acids is present

CC between HuEPO and human Igg Fc variant, and the HuEPO-L-vFc fusion

CC protein exhibits in vitro biological activity similar to or higher than

CC that of rHuEPO on a molar basis. Preferred Method: Making a recombinant

CC fusion protein comprising HuEPO, a flexible peptide linker, and a human

CC Igg Fc variant comprises: generating a CHO-derived cell line; growing the

CC cell line where the recombinant protein is expressed in its growth medium

CC in excess of 10 μ mol/g per million cells in a 24 hour period; and

CC purifying the expressed protein from (b), where the recombinant fusion

CC protein exhibits in vitro biological activity similar to or higher than

CC that of rHuEPO on a molar basis. Antianemic; Nephrotropic. No biological

CC data given. None given. Administration can be through subcutaneous or

CC intravenous route. No dosage given. The recombinant HuEPO-L-vFc fusion

CC protein is useful for treating patients with chronic anemia due to renal

CC diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for

CC HIV infection, or myelodysplastic syndrome. It is also useful in the

CC treatment of renal failure. A fusion protein was assembled from several

CC DNA segments. To obtain the gene encoding the leader peptide and mature

CC protein of human erythropoietin (EPO), cDNA library of human fetal liver

CC or kidney was used as the template in polymerase chain reaction (PCR).

CC For the convenience of cloning, SEQ ID NO. 1 which incorporates a

CC restriction enzyme cleavage site is used as the 5' oligonucleotide

CC primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon

CC and incorporates a BamHI site. The resulting DNA fragments of

CC approximately 600 bp were inserted into a holding vector such as pUC19 at

CC the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the

CC human EPO gene was confirmed by DNA sequencing.

XX Sequence 29 BP; 9 A; 12 C; 5 G; 3 T; 0 U; 0 Other;

Qy Query Match 74.0%; Score 14.8; DB 13; Length 29;

Db Best Local Similarity 77.8%; Pred. No. 2.8e+03;

Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCGGGAGGCCU 19

Db 18 ATGGAGGCTGGGAGGCCT 1


```
RESULT 17
ACD65499
ID ACD65499 standard; RNA; 17 BP.
XX AC ACD65499;
XX AC ACD65499;
XX 30-SEP-2003 (first entry)
XX HCV minus strand DNazyme substrate sequence #2074.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
XX amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.
XX
XX Hepatitis C virus.
XX
XX WO200281494-A1.
XX
XX 17-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009187.
XX
XX 26-MAR-2001; 2001US-00817879.
XX 08-JUN-2001; 2001US-00877478.
XX 08-JUN-2001; 2001US-0296876P.
XX 24-OCT-2001; 2001US-0335059P.
XX 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MACE/) MACEJAK D.
XX (MCSW/) MCSWIGGEN J.
XX (MORR/) MORRISSEY D.
XX (PAVC/) PAVCO P.
XX (LEEP/) LEE P.
XX (DRAP/) DRAPER K.
XX (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
XX Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
XX hepatocellular carcinoma, or condition associated with hepatitis C virus
XX infection.
XX
XX Claim 1; Page 312; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
XX inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX as oligonucleotides that specifically bind the Enhancer I region of HBV
XX DNA. The nucleic acids may be used to modulate the expression of HBV
XX genes and HBV viral replication. Also disclosed is a method for screening
XX compounds and/or potential therapies directed against HBV, and compounds
XX that modulate the expression and/or replication of HCV. The compounds and
XX methods of the invention are useful for the treatment of degenerative and
XX disease states related to HBV and HCV infection, replication and gene
XX expression such as cirrhosis, liver failure, and hepatocellular
XX carcinoma. The present sequence represents a substrate for one of the HCV
XX DNazyme or minus strand DNazyme sequences disclosed in the present
XX invention
```

```
XX
XX Sequence 17 BP; 4 A; 2 C; 9 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 72.0%; Score 14.4; DB 8; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 4.3e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 AACGGAGGCGUGGAUG 16
XX 2 ACCGGAGGCGUGGAUG 17
XX
XX RESULT 18
XX ACD57170/c
XX ID ACD57170 standard; RNA; 17 BP.
XX AC ACD57170;
XX 23-SEP-2003 (first entry)
XX
XX HCV DNazyme substrate sequence #204.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
XX amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.
XX
XX Hepatitis C virus.
XX
XX WO200281494-A1.
XX
XX 17-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009187.
XX
XX 26-MAR-2001; 2001US-00817879.
XX 08-JUN-2001; 2001US-00877478.
XX 08-JUN-2001; 2001US-0296876P.
XX 24-OCT-2001; 2001US-0335059P.
XX 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MACE/) MACEJAK D.
XX (MCSW/) MCSWIGGEN J.
XX (MORR/) MORRISSEY D.
XX (PAVC/) PAVCO P.
XX (LEEP/) LEE P.
XX (DRAP/) DRAPER K.
XX (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
XX Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
XX hepatocellular carcinoma, or condition associated with hepatitis C virus
XX infection.
XX
XX Claim 1; Page 237; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
XX inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX as oligonucleotides that specifically bind the Enhancer I region of HBV
XX DNA. The nucleic acids may be used to modulate the expression of HBV
XX genes and HBV viral replication. Also disclosed is a method for screening
XX compounds and/or potential therapies directed against HBV, and compounds
XX that modulate the expression and/or replication of HCV. The compounds and
XX methods of the invention are useful for the treatment of degenerative and
XX disease states related to HBV and HCV infection, replication and gene
XX expression such as cirrhosis, liver failure, and hepatocellular
XX carcinoma. The present sequence represents a substrate for one of the HCV
XX DNazyme or minus strand DNazyme sequences disclosed in the present
XX invention
```


CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNzyme or minus strand DNzyme sequences disclosed in the present
 CC invention
 XX
 SQ Sequence 17 BP; 2 A; 10 C; 2 G; 0 T; 3 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 8; Length 17;
 Best Local Similarity 81.2%; Pred. No. 4.3e+03;
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUG 16
 | | | | | | | | | | | | | | | | | |
 Db 17 AGCGGAGGCTGGGATG 2

RESULT 19
 ADI87105
 ID ADI87105 standard; RNA; 17 BP.
 XX
 AC ADI87105;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE HCV DNzyme substrate sequence #4351.
 XX
 KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
 KW HCV infection; type I interferon; DNzyme.
 XX
 OS Hepatitis C virus.
 XX
 PN US2003125270-A1.
 XX
 PD 03-JUL-2003.
 XX
 PF 18-DEC-2000; 2000US-00740332.
 XX
 PR 18-DEC-2000; 2000US-00740332.
 XX
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (ROBE/) ROBERTS E.
 PA (PAVC/) PAVCO P A.
 PA (MACE/) MACEJACK D.
 XX
 PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
 XX
 WPI; 2004-031273/03.
 XX
 PT Enzymatic nucleic acid molecules which specifically cleave RNA derived
 PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
 PT especially in combination with type I interferon therapy.
 XX
 PS Claim 1; SEQ ID NO 4351; 198pp; English.

CC The invention relates to an enzymatic nucleic acid molecule which
 CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
 CC the binding arms of the enzymatic nucleic acid molecule comprises
 CC sequences complementary to any of the defined substrate sequences given
 CC in the specification. The nucleic acid molecule may be administered for
 CC the treatment of HCV infections, especially in combination with type I
 CC interferons. The present sequence represents a HCV DNzyme substrate
 CC sequence.
 XX
 SQ Sequence 17 BP; 4 A; 2 C; 9 G; 0 T; 2 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 12; Length 17;
 Best Local Similarity 93.8%; Pred. No. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AACGGAGGCGGGAUG 16
 | | | | | | | | | | | | | | | | | |
 Db 2 AGCGGAGGCGGGAUG 17

RESULT 20
 ADI82958/c
 ID ADI82958 standard; RNA; 17 BP.
 XX
 AC ADI82958;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE HCV DNzyme substrate sequence #204.
 XX
 KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
 KW HCV infection; type I interferon; DNzyme.
 XX
 OS Hepatitis C virus.
 XX
 PN US2003125270-A1.
 XX
 PD 03-JUL-2003.
 XX
 PF 18-DEC-2000; 2000US-00740332.
 XX
 PR 18-DEC-2000; 2000US-00740332.
 XX
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (ROBE/) ROBERTS E.
 PA (PAVC/) PAVCO P A.
 PA (MACE/) MACEJACK D.
 XX
 PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
 XX
 WPI; 2004-031273/03.
 XX
 PT Enzymatic nucleic acid molecules which specifically cleave RNA derived
 PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
 PT especially in combination with type I interferon therapy.
 XX
 PS Claim 1; SEQ ID NO 204; 198pp; English.

CC The invention relates to an enzymatic nucleic acid molecule which
 CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
 CC the binding arms of the enzymatic nucleic acid molecule comprises
 CC sequences complementary to any of the defined substrate sequences given
 CC in the specification. The nucleic acid molecule may be administered for
 CC the treatment of HCV infections, especially in combination with type I
 CC interferons. The present sequence represents a HCV DNzyme substrate
 CC sequence.
 XX
 SQ Sequence 17 BP; 2 A; 10 C; 2 G; 0 T; 3 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 12; Length 17;
 Best Local Similarity 81.2%; Pred. No. 4.3e+03;
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUG 16
 | | | | | | | | | | | | | | | | | |
 Db 17 AGCGGAGGCTGGGATG 2

RESULT 21
 AAA63817/c
 ID AAA63817 standard; DNA; 26 BP.
 XX
 AC AAA63817;

CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX
SQ Sequence 41 BP; 5 A; 18 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 6; Length 41;
Best Local Similarity 65.0%; Pred. NO. 1.1e+04;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUCCUU 20
Db | ||||| : ||| :
18 ACCGGAGCCTGGGGTGCCT 37

Search completed: May 24, 2005, 10:21:26
Job time : 439 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 07:28:20 ; Search time 2987 Seconds
(without alignments)
254.866 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacggagcgggaugccuu 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gest1.*
- 9: gb_gest2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.2	66.0	50	1	AU105005
2	12.6	63.0	25	6	C01243
3	12.6	63.0	42	9	AL762172 Arabidops
4	12.6	63.0	49	8	AZ355782
5	12.4	62.0	40	7	R71941
6	12.2	61.0	30	8	AZ360543
7	12.2	61.0	32	8	AZ451624
8	12.2	61.0	37	9	CG426451
9	12.2	61.0	39	9	CL436595
10	12.2	61.0	48	8	CC325220
11	12.2	61.0	49	1	AI889596
12	12.2	61.0	50	1	AU106001
13	12.2	61.0	50	1	AU106002
14	12.2	61.0	50	1	AU106005
15	12.2	61.0	50	1	AU106010
16	12.2	61.0	50	1	AU106011
17	12.2	61.0	50	1	AU106012
18	12.2	61.0	50	1	AU106013
19	12.2	61.0	50	1	AU106014
20	12.2	61.0	43	7	H41392
21	12.2	60.0	49	8	BH907010
22	12.2	60.0	49	8	BX661683
23	11.8	59.0	36	7	N50146
24	11.8	59.0	42	8	CC326042

```

98 10.8 54.0 43 7 H45703
99 10.8 54.0 45 4 BM397811 5009-0-37
100 10.8 54.0 46 1 AI096136 SNOV13CAN
101 10.8 54.0 46 1 AI863959 WJ54A06.X
102 10.8 54.0 46 9 BX122407 Danio rer
103 10.8 54.0 46 9 CL983238 GC0477 TI
104 10.8 54.0 50 1 AU104812 AU104812
105 10.8 54.0 50 1 AU105802 AU105802
106 10.8 54.0 50 1 AU107291 AU107291
107 10.8 54.0 50 1 AU107830 AU107830
108 10.6 53.0 28 1 AJ747388 AU747388
109 10.6 53.0 30 9 TA197G11Q
110 10.6 53.0 31 1 AI422071 tf57e03.x
111 10.6 53.0 32 9 CG707593 1119003A1
112 10.6 53.0 35 4 BI668131 603295966
113 10.6 53.0 35 7 T74041 YC55C08.S1
114 10.6 53.0 36 7 CO794014 NT0198.G0
115 10.6 53.0 37 7 N47919 YW97C12.F1
116 10.6 53.0 38 8 AZ758198 IM0550P03
117 10.6 53.0 38 8 BH129371 G-5b8.f.M
118 10.6 53.0 41 8 AZ480375 IM0301A20
119 10.6 53.0 41 8 BH26532 100711080
120 10.6 53.0 42 8 BH624960 1007091C0
121 10.6 53.0 42 8 BH840598 KG05760-3
122 10.6 53.0 43 1 AI783492 kz36a07.x
123 10.6 53.0 43 9 TA84B02Q AU105809
124 10.6 53.0 43 9 CL303156 G068D06.G
125 10.6 53.0 44 8 AZ347569 IM0083P11
126 10.6 53.0 46 1 AA649959 nb55d03.s
127 10.6 53.0 46 4 BI408611 602963504
128 10.6 53.0 46 9 CG785232 OOS0119-0
129 10.6 53.0 47 8 AZ379524 IM0134E16
130 10.6 53.0 47 9 TA100F09Q
131 10.6 53.0 48 8 CC199771 KH136.Bay
132 10.6 53.0 50 1 AU103167 AU103167
133 10.6 53.0 50 1 AU105807 AU105807
134 10.6 53.0 50 1 AU105809 AU105809
135 10.6 53.0 50 1 AU105810 AU105810
136 10.6 53.0 50 1 AU105811 AU105811
137 10.6 53.0 50 1 AU105812 AU105812
138 10.6 53.0 50 1 AU105814 AU105814
139 10.6 53.0 50 1 AU105818 AU105818
140 10.6 53.0 50 1 AU105819 AU105819
141 10.6 53.0 50 1 AU105820 AU105820
142 10.6 53.0 50 1 AU105825 AU105825
143 10.6 53.0 50 1 AU106003 AU106003
144 10.6 53.0 50 1 AU106928 AU106928
145 10.6 53.0 50 1 AU107644 AU107644
146 10.6 53.0 50 8 AZ777046 2M0011M08
147 10.6 53.0 50 9 CG672135 RRN226.Ba
148 10.6 53.0 50 9 CL437014 PST4323-N
149 10.4 52.0 22 8 AZ864977 2M0174D21
150 10.4 52.0 25 8 AZ815351 2M0083102

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ALIGNMENTS

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RESULT 1
AUI05005 50 bp mRNA linear EST 28-VAN-2004
LOCUS ADS01748, mRNA sequence.
DEFINITION AUI05005 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AUI05005.1 GI:13554526
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ORGANISM
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,

```

```

TITLE Sakai.Y., Nakamura.Y., Suyama.A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ms.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             Location/Qualifiers
     source            1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="ADS01748"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      66.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGGAGGCGUGGAUGCCUU 20
    ||| ||||| |||:
Db 15 CGGCGTCTGGGAGGCGCTT 32

RESULT 2
C01243
LOCUS HUMG0007966 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
DEFINITION
ACCESSION C01243
VERSION C01243.1 GI:14333473
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 25)
AUTHORS Okubo,K.
TITLE BodyMap; human gene expression database
JOURNAL Unpublished (1995)
COMMENT Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see , http://www.imcb.osaka-u.ac.jp/bodymap/. The
sequences of the clones represented by this GS sequences is also
found there.
FEATURES             Location/Qualifiers
     source            1..25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="adult"
                     /clone_lib="Human adult (K.Okubo)"
                     /note="One or more human adult tissue"
ORIGIN
Query Match      63.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 68.4%; Pred. No. 2.2e+05;

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Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACGGAGCGGGAUGCCU 19
 ||||| :|||
 Db 7 AAGGAGCGAGGTTTGCCT 25

RESULT 3
 AL762172/c
 LOCUS
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-021E05-013692, genomic survey sequence.

ACCESSION AL762172
 VERSION AL762172.1 GI:21506882
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE 1
 Li.Y., Rosso.M.G., Strizhov.N., Viehoever.P. and Weissshaar.B.
 GABI-Kat SimpleSearch: a flanking sequence tag (PST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
 Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL MEDLINE
 PUBMED 22755829
 PUBMED 12874060

REFERENCE 2
 Rosso.M.G., Li.Y., Strizhov.N., Reiss.B., Dekker.K. and Weissshaar.B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)

JOURNAL MEDLINE
 PUBMED 23117147
 PUBMED 14756321

REFERENCE 3
 Strizhov.N., Li.Y., Rosso.M.G., Viehoever.P., Dekker.K.A. and Weissshaar.B.
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
 Biotechniques 35 (6), 1164-1168 (2003)

JOURNAL PUBMED
 14682050
 REFERENCE 4 (bases 1 to 42)
 Li.Y., Strizhov.N., Rosso.M.G. and Weissshaar.B.

TITLE Direct Submission
 Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At2g47140. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
 source
 1..42
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clones="GK-021E05-013692"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC106 (GenBank accession number: AJ537513). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

ORIGIN

Query Match 63.0%; Score 12.6; DB 9; Length 42;
 Best Local Similarity 63.2%; Pred. No. 2.4e+05;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACGGAGCGGGAUGCCUU 20
 ||||| :|||
 Db 28 ATGGAGCGCGGATGCCTT 10

RESULT 4
 AZ355782/c
 LOCUS
 DEFINITION AZ355782 49 bp DNA linear GSS 02-OCT-2000
 clone UUGC1M0095B09 R, genomic survey sequence.

ACCESSION AZ355782
 VERSION AZ355782.1 GI:10468447
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 49)

REFERENCE 1
 Dunn.D., Aoyagi.A., Barber.M., Beacorn.T., Duval.B., Hamil.C., Irlam.H., Longacre.S., Mahmoud.M., Meenen.E., Pedersen.I., Reilly.M., Rose.M., Rose.R., Stokes.R., Tingey.A., von Niederhausern.A. and Wright.D., Weiss.R.
 Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts
 Unpublished (2000)

JOURNAL COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0095 row: B column: 09

Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 49.

FEATURES
 source
 1..49
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clones="UUGC1M0095B09"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10Kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114[GB|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 63.0%; Score 12.6; DB 8; Length 49;
 Best Local Similarity 63.2%; Pred. No. 2.4e+05;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCU 19
 || |||||:|:|:|:
 Db 48 AAAAGAGGTGAGATGCT 30

RESULT 5
 R71941/c
 LOCUS
 DEFINITION
 Y184a06.r1 Soares breast 2NBHbSt Homo sapiens cDNA clone
 IMAGE:155410.5' similar to SP:A48528 S36556; MEMBRANE GLYCOPROTEIN
 CLA-1 PROTEIN LONG FORM PRECURSOR - ;, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

R71941
 Homo sapiens (human)
 EST.
 EST.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 40)
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevisakis,B., Waterston,K., Williamson,A., Wohlmann,P. and
 Wilson,R.

TITLE
 JOURNAL
 COMMENT

The WashU-Merck EST Project
 Unpublished (1995)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

Insert Size: 2714
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LiML; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Insert length: 2714 Std Error: 0.00
 Seq primer: M13RP1
 High quality sequence stop: 1.

FEATURES
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Location/Qualifiers
 1..40
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:573028"
 /db_xref="taxon:9606"
 /clone="IMAGE:155410"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares breast 2NBHbSt"
 /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTACCATCTGAGTGGGAGCGCGCCCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of a modified pT7T3 vector (Pharmacia).
 Library went through one round of normalization to a Cot =
 230. Library constructed by Bento Soares and M. Fatima
 Bonaudo."

ORIGIN

Query Match 62.0%; Score 12.4; DB 7; Length 40;
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;

Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 6 AGGCGUGGAGCCUU 20
 ||| |||||:|:|:|:
 Db 38 AGGCGGATGCCIT 24

RESULT 6
 A2360543
 LOCUS
 DEFINITION
 IM0103004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0103004 R, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

A2360543.1 GI:10474243
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 30)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Isiam,H., Longacre,S., Mamoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0103 row: O column: 04
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 30.

FEATURES
 source

Location/Qualifiers
 1..30
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0103004"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 61.0%; Score 12.2; DB 8; Length 30;
 Best Local Similarity 58.8%; Pred. No. 3.5e+05;

Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGAGGCGGGAUGCCUU 20
 ||| :|||||:
 Db 7 GGGCTTGGGATGCTT 23

RESULT 7
 AZ451624
 LOCUS
 DEFINITION
 Clone UUGC1M0251O06 F, genomic survey sequence.

ACCESSION
 AZ451624
 VERSION
 AZ451624.1 GI:10607615
 KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
 1 (bases 1 to 32)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

TELEPHONE
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0251 row: 0 column: 06

Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends

High quality sequence stop: 32.

FEATURES
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 1..32
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0251O06"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 cf PWD42 [GI4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 61.0%; Score 12.2; DB 8; Length 32;
 Best Local Similarity 58.8%; Pred. No. 3.6e+05;

Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGAGGCGGGAUGCCUU 20
 ||| :|||||:
 Db 7 GGATGGTGGATACCTT 23

RESULT 8
 CG426451
 LOCUS
 DEFINITION
 01S0586-03B1-F06 UniformMu MutTAIL Library Zea mays genomic clone

ACCESSION
 CG426451
 VERSION
 CG426451.1 GI:34734931
 KEYWORDS
 GSS.

SOURCE
 Zea mays
 ORGANISM
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
 1 (bases 1 to 37)
 Latshaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
 Sequence tagged transposon insertions from the UniformMu maize
 population

JOURNAL
 COMMENT
 Unpublished (2003)
 Contact: Donald R. McCarty
 Plant Molecular and Cellular Biology Program
 University of Florida
 PO 110690 Gainesville, FL 32611-0690, USA

TELEPHONE
 Tel: 352-392-1928 x322
 Email: drmc@ufl.edu
 Sequence flanking probable Mu insertion site in UniformMu line:
 01S0586-03, Primer set: B

Class: transposon insertion site.

FEATURES
 source
 1..37
 Location/Qualifiers

/organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="W22 (ACR, bz1-m9)"
 /cultivar="UniformMu"
 /db_xref="taxon:4577"
 /clone="01S0586-03B1-F06"
 /clone_lib="UniformMu MutTAIL Library"
 /notes="Vector: TOPO-PCR4; DNA flanking Mu transposon
 insertions in Mu inactive lines were extracted from the
 UniformMu maize population by the thermo asymmetric
 interlaced PCR (TAIL) protocol using primers specific for
 the Mu terminal inverted repeat and a set of 16 arbitrary
 primers. Amplicons were size enriched using Sepharose 400
 spin columns and cloned into the TOPO PCR4 vector."

ORIGIN

Query Match 61.0%; Score 12.2; DB 9; Length 37;
 Best Local Similarity 76.8%; Pred. No. 3.6e+05;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGC 17
 ||| :|||||:
 Db 6 ATGGAGGCGGGGATTC 22

RESULT 9
 CL436595/c
 LOCUS
 DEFINITION
 PST3320-NR.Seq MICH1 Mus musculus genomic clone PST3320-NR.Seq,
 genomic survey sequence.

ACCESSION
 CL436595
 VERSION
 CL436595.1 GI:45571546
 KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE
AUTHORS      1 (bases 1 to 39)
TITLE        Hicks,G.G.
JOURNAL      www.EScells.ca
COMMENT      Unpublished (2002)
             Contact: Hicks GG
             Mammalian Functional Genomics Centre
             Manitoba Institute of Cell Biology, University of Manitoba
             ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
             Tel: 204 787 2133
             Fax: 204 787 2190
             Email: hicks@gcc.umanitoba.ca
             U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
             sequence information and target gene cloning can be generated. ES
             cell line harboring insertion mutation of target gene is available.
             Sequence analysis available from
             http://140.193.242.7/esdb/public_search_frame.php?PST=PST3320-NR.Se
             q
Class: Gene Trap.
          Location/Qualifiers
          1..39
             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="129 sv"
             /db_xref="taxon:10090"
             /clone="PST3320-NR.Seq"
             /sex="Male"
             /cell_type="Embryonic stem cell"
             /cell_line="D3H (J1 subclone)"
             /clone_lib="M1CB1"
             /note="Vector: U3NeoSV1"

ORIGIN
Query Match      61.0%; Score 12.2; DB 9; Length 39;
Best Local Similarity 76.5%; Pred. No. 3.6e+05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AACGGAGGCGGGAUGC 17
        ||| ||||| |||||
Db      23 AAGGAGGCTGGGAGGC 7

RESULT 10
CC325220/c
LOCUS      CC325220
DEFINITION CC325220 BayGenomics Gene Trap Library pGT0Lxf Mus musculus cDNA, mRNA
sequence.
ACCESSION CC325220
VERSION   CC325220.1 GI:30719278
KEYWORDS GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 48)
AUTHORS    BayGenomics.
TITLE      http://baygenomics.ucsf.edu/
JOURNAL    Unpublished (2001)
COMMENT    Contact: BayGenomics
            Bay Area Functional Genomics Consortium (BayGenomics)
            Email: info@baygenomics.ucsf.edu
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from BayGenomics. Annotation
            information available from
            http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
            CELL_LINE&KEY=XM220
Class: Gene Trap.
          Location/Qualifiers
          1..48
             /organism="Mus musculus"
             /mol_type="mRNA"
             /strain="129 ola"
             /db_xref="taxon:10090"

FEATURES
source
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             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:2440230"
             /tissue_type="moderately-differentiated endometrial
             adenocarcinoma, 3 pooled tumors"
             /lab_host="DH10B"
             /clone_lib="NCI CGAP Ut2"
             /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
             Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
             Average insert size 1.85 kb. Life Technologies catalog #:
             11539-012"

REFERENCE
AUTHORS      1 (bases 1 to 39)
TITLE        Hicks,G.G.
JOURNAL      www.EScells.ca
COMMENT      Unpublished (2002)
             Contact: Hicks GG
             Mammalian Functional Genomics Centre
             Manitoba Institute of Cell Biology, University of Manitoba
             ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
             Tel: 204 787 2133
             Fax: 204 787 2190
             Email: hicks@gcc.umanitoba.ca
             U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
             sequence information and target gene cloning can be generated. ES
             cell line harboring insertion mutation of target gene is available.
             Sequence analysis available from
             http://140.193.242.7/esdb/public_search_frame.php?PST=PST3320-NR.Se
             q
Class: Gene Trap.
          Location/Qualifiers
          1..39
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             /strain="129 sv"
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             /clone="PST3320-NR.Seq"
             /sex="Male"
             /cell_type="Embryonic stem cell"
             /cell_line="D3H (J1 subclone)"
             /clone_lib="M1CB1"
             /note="Vector: U3NeoSV1"

ORIGIN
Query Match      61.0%; Score 12.2; DB 9; Length 39;
Best Local Similarity 76.5%; Pred. No. 3.6e+05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AACGGAGGCGGGAUGC 17
        ||| ||||| |||||
Db      23 AAGGAGGCTGGGAGGC 7

RESULT 10
CC325220/c
LOCUS      CC325220
DEFINITION CC325220 BayGenomics Gene Trap Library pGT0Lxf Mus musculus cDNA, mRNA
sequence.
ACCESSION CC325220
VERSION   CC325220.1 GI:30719278
KEYWORDS GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 48)
AUTHORS    BayGenomics.
TITLE      http://baygenomics.ucsf.edu/
JOURNAL    Unpublished (2001)
COMMENT    Contact: BayGenomics
            Bay Area Functional Genomics Consortium (BayGenomics)
            Email: info@baygenomics.ucsf.edu
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from BayGenomics. Annotation
            information available from
            http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
            CELL_LINE&KEY=XM220
Class: Gene Trap.
          Location/Qualifiers
          1..48
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             /mol_type="mRNA"
             /strain="129 ola"
             /db_xref="taxon:10090"

FEATURES
source
          1..48
             /organism="Mus musculus"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:2440230"
             /tissue_type="moderately-differentiated endometrial
             adenocarcinoma, 3 pooled tumors"
             /lab_host="DH10B"
             /clone_lib="NCI CGAP Ut2"
             /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
             Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
             Average insert size 1.85 kb. Life Technologies catalog #:
             11539-012"

REFERENCE
AUTHORS      1 (bases 1 to 39)
TITLE        Hicks,G.G.
JOURNAL      www.EScells.ca
COMMENT      Unpublished (2002)
             Contact: Hicks GG
             Mammalian Functional Genomics Centre
             Manitoba Institute of Cell Biology, University of Manitoba
             ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
             Tel: 204 787 2133
             Fax: 204 787 2190
             Email: hicks@gcc.umanitoba.ca
             U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
             sequence information and target gene cloning can be generated. ES
             cell line harboring insertion mutation of target gene is available.
             Sequence analysis available from
             http://140.193.242.7/esdb/public_search_frame.php?PST=PST3320-NR.Se
             q
Class: Gene Trap.
          Location/Qualifiers
          1..39
             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="129 sv"
             /db_xref="taxon:10090"
             /clone="PST3320-NR.Seq"
             /sex="Male"
             /cell_type="Embryonic stem cell"
             /cell_line="D3H (J1 subclone)"
             /clone_lib="M1CB1"
             /note="Vector: U3NeoSV1"

ORIGIN
Query Match      61.0%; Score 12.2; DB 8; Length 48;
Best Local Similarity 70.6%; Pred. No. 3.7e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      2 ACGGAGGCGGGAUCC 18
        ||||| |||||
Db      28 ACGGAGGCTGGACTCC 12

RESULT 11
AI889596
LOCUS      AI889596
DEFINITION AI889596
similar to SW:GCI_HUMAN P01857 IG GAMMA-1 CHAIN C REGION. ;, mRNA
sequence.
ACCESSION AI889596
VERSION   AI889596.1 GI:5594760
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 49)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapsb-remail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 2514 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
            Location/Qualifiers
            1..49
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:2440230"
               /tissue_type="moderately-differentiated endometrial
               adenocarcinoma, 3 pooled tumors"
               /lab_host="DH10B"
               /clone_lib="NCI CGAP Ut2"
               /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
               Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 1.85 kb. Life Technologies catalog #:
               11539-012"

REFERENCE
AUTHORS      1 (bases 1 to 39)
TITLE        Hicks,G.G.
JOURNAL      www.EScells.ca
COMMENT      Unpublished (2002)
             Contact: Hicks GG
             Mammalian Functional Genomics Centre
             Manitoba Institute of Cell Biology, University of Manitoba
             ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
             Tel: 204 787 2133
             Fax: 204 787 2190
             Email: hicks@gcc.umanitoba.ca
             U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
             sequence information and target gene cloning can be generated. ES
             cell line harboring insertion mutation of target gene is available.
             Sequence analysis available from
             http://140.193.242.7/esdb/public_search_frame.php?PST=PST3320-NR.Se
             q
Class: Gene Trap.
          Location/Qualifiers
          1..39
             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="129 sv"
             /db_xref="taxon:10090"
             /clone="PST3320-NR.Seq"
             /sex="Male"
             /cell_type="Embryonic stem cell"
             /cell_line="D3H (J1 subclone)"
             /clone_lib="M1CB1"
             /note="Vector: U3NeoSV1"

ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 49;
Best Local Similarity 70.6%; Pred. No. 3.7e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GGAGGCGGGAUCCUU 20
        ||||| |||||
Db      31 GGGGCGCGGAGCCTT 47

RESULT 12
AU106001

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/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"
/note="Vector: pGT0Lxf"

ORIGIN
Query Match      61.0%; Score 12.2; DB 8; Length 48;
Best Local Similarity 70.6%; Pred. No. 3.7e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      2 ACGGAGGCGGGAUCC 18
        ||||| |||||
Db      28 ACGGAGGCTGGACTCC 12

RESULT 11
AI889596
LOCUS      AI889596
DEFINITION AI889596
similar to SW:GCI_HUMAN P01857 IG GAMMA-1 CHAIN C REGION. ;, mRNA
sequence.
ACCESSION AI889596
VERSION   AI889596.1 GI:5594760
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 49)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapsb-remail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 2514 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
            Location/Qualifiers
            1..49
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:2440230"
               /tissue_type="moderately-differentiated endometrial
               adenocarcinoma, 3 pooled tumors"
               /lab_host="DH10B"
               /clone_lib="NCI CGAP Ut2"
               /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
               Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 1.85 kb. Life Technologies catalog #:
               11539-012"

REFERENCE
AUTHORS      1 (bases 1 to 39)
TITLE        Hicks,G.G.
JOURNAL      www.EScells.ca
COMMENT      Unpublished (2002)
             Contact: Hicks GG
             Mammalian Functional Genomics Centre
             Manitoba Institute of Cell Biology, University of Manitoba
             ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
             Tel: 204 787 2133
             Fax: 204 787 2190
             Email: hicks@gcc.umanitoba.ca
             U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
             sequence information and target gene cloning can be generated. ES
             cell line harboring insertion mutation of target gene is available.
             Sequence analysis available from
             http://140.193.242.7/esdb/public_search_frame.php?PST=PST3320-NR.Se
             q
Class: Gene Trap.
          Location/Qualifiers
          1..39
             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="129 sv"
             /db_xref="taxon:10090"
             /clone="PST3320-NR.Seq"
             /sex="Male"
             /cell_type="Embryonic stem cell"
             /cell_line="D3H (J1 subclone)"
             /clone_lib="M1CB1"
             /note="Vector: U3NeoSV1"

ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 49;
Best Local Similarity 70.6%; Pred. No. 3.7e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GGAGGCGGGAUCCUU 20
        ||||| |||||
Db      31 GGGGCGCGGAGCCTT 47

RESULT 12
AU106001

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LOCUS       AU106001          50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION   AU106001 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
              HEP01436, mRNA sequence.
ACCESSION    AU106001
VERSION      AU106001.1 GI:13555522
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 50)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
              Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
              ENBO Rep. 2 (5), 388-393 (2001)
              21270072
              PUBMED 11375929
              CONTACT: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yuzuki@ims.u-tokyo.ac.jp
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).
FEATURES             Location/Qualifiers
     source         1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Sugano Homo sapiens cDNA library"
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Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGNAUC 17
        |||||:||||:|
Db      16 AGCGGTGGCTGGGCTGC 32

RESULT 13
LOCUS     AU106002          50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION   AU106002 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
              HEP03378, mRNA sequence.
ACCESSION    AU106002
VERSION      AU106002.1 GI:13555523
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 50)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
              Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
              ENBO Rep. 2 (5), 388-393 (2001)
              21270072
              PUBMED 11375929
              CONTACT: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).
FEATURES             Location/Qualifiers
     source         1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Sugano Homo sapiens cDNA library"
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Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGNAUC 17
        |||||:||||:|
Db      17 AGCGGTGGCTGGGCTGC 33

RESULT 13
LOCUS     AU106001          50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION   AU106001 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
              HEP01436, mRNA sequence.
ACCESSION    AU106001
VERSION      AU106001.1 GI:13555522
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 50)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
              Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
              ENBO Rep. 2 (5), 388-393 (2001)
              21270072
              PUBMED 11375929
              CONTACT: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).
FEATURES             Location/Qualifiers
     source         1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGNAUC 17
        |||||:||||:|
Db      16 AGCGGTGGCTGGGCTGC 32

RESULT 14
LOCUS     AU106005          50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION   AU106005 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
              HEP09434, mRNA sequence.
ACCESSION    AU106005
VERSION      AU106005.1 GI:13555526
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 50)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
              Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
              ENBO Rep. 2 (5), 388-393 (2001)
              21270072
              PUBMED 11375929
              CONTACT: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).
FEATURES             Location/Qualifiers
     source         1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGNAUC 17
        |||||:||||:|
Db      17 AGCGGTGGCTGGGCTGC 33

RESULT 15
LOCUS     AU106010          50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION   AU106010 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
              HEP09434, mRNA sequence.
ACCESSION    AU106010
VERSION      AU106010.1 GI:13555527
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 50)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
              Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
              ENBO Rep. 2 (5), 388-393 (2001)
              21270072
              PUBMED 11375929
              CONTACT: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).
FEATURES             Location/Qualifiers
     source         1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGNAUC 17
        |||||:||||:|
Db      17 AGCGGTGGCTGGGCTGC 33

```

```

LNG08752, mRNA sequence.
ACCESSION      AUI06010
VERSION        AUI06010.1  GI:13555531
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               1 (bases 1 to 50)
               Hata,H., Ota,T., Isogai,T., Tanaka,T., Mizushima-Sugano,J., Sese,J.,
               Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE         Diverse transcriptional initiation revealed by fine, large-scale
               mapping of mRNA start sites
JOURNAL       EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE       21270072
PUBMED        11375929
COMMENT       Contact: Yutaka Suzuki
               Department of Virology
               Institute of Medical Science, University of Tokyo
               4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
               Email: ysuzuki@ims.u-tokyo.ac.jp
               Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
               Sugano,S. Construction and characterization of a full
               length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
               149-156 (1997).

FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="LNG08752"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

     1 AACGGAGGCGUGGAUGC 17
     |||||:||||:||||
     17 AGCGGTGGCTGGCGTGC 33

RESULT 16
LOCUS      AUI06011
DEFINITION AUI06011 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
           KAI040044, mRNA sequence.
ACCESSION  AUI06011
VERSION    AUI06011.1  GI:13555532
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           1 (bases 1 to 50)
           Hata,H., Ota,T., Isogai,T., Tanaka,T., Mizushima-Sugano,J., Sese,J.,
           Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE      Diverse transcriptional initiation revealed by fine, large-scale
           mapping of mRNA start sites
JOURNAL    EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE    21270072
PUBMED     11375929
COMMENT    Contact: Yutaka Suzuki
           Department of Virology
           Institute of Medical Science, University of Tokyo
           4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
           Email: ysuzuki@ims.u-tokyo.ac.jp
           Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
           Sugano,S. Construction and characterization of a full
           length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
           149-156 (1997).

```

```

149-156 (1997).
FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="KAI040044"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

     1 AACGGAGGCGUGGAUGC 17
     |||||:||||:||||
     16 AGCGGTGGCTGGCGTGC 32

RESULT 17
LOCUS      AUI06012
DEFINITION AUI06012 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
           KAI0733, mRNA sequence.
ACCESSION  AUI06012
VERSION    AUI06012.1  GI:13555533
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           1 (bases 1 to 50)
           Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
           Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
           Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE      Diverse transcriptional initiation revealed by fine, large-scale
           mapping of mRNA start sites
JOURNAL    EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE    21270072
PUBMED     11375929
COMMENT    Contact: Yutaka Suzuki
           Department of Virology
           Institute of Medical Science, University of Tokyo
           4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
           Email: ysuzuki@ims.u-tokyo.ac.jp
           Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
           Sugano,S. Construction and characterization of a full
           length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
           149-156 (1997).

FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="KAI0733"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

     1 AACGGAGGCGUGGAUGC 17
     |||||:||||:||||
     28 AGCGGTGGCTGGCGTGC 44

RESULT 18
LOCUS      AUI06013
DEFINITION AUI06013 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
           KAI05020, mRNA sequence.
ACCESSION  AUI06013

```


(pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

ORIGIN

Query Match 60.0%; Score 12; DB 7; Length 43;
 Best Local Similarity 60.0%; Pred. No. 4.6e+05;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AACGAGGCGGGAUGCCUU 20
 |||||:|:|:|:
 Db 2 AATGACGCGCGGATGCTT 21

RESULT 21

BH907010/c
 LOCUS
 DEFINITION 48 bp DNA linear GSS 04-SEP-2002
 SALK_037281.30.90.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_037281.30.90.x, genomic survey sequence.

ACCESSION

BH907010
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 48)
 Alonso,J.M., Leishe,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker

JOURNAL

COMMENT
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379

Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At3g58820.
 Class: TDNA tagged.

FEATURES

source

Location/Qualifiers

1..48
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_037281.30.90.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 60.0%; Score 12; DB 8; Length 48;
 Best Local Similarity 55.0%; Pred. No. 4.6e+05;
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy

1 AACGAGGCGGGAUGCCUU 20

Db

20 AAAGGAGGCTGCTTGACTT 1

RESULT 22

BX661683
 LOCUS
 DEFINITION 49 bp DNA linear GSS 05-APR-2004
 Arabidopsis thaliana T-DNA flanking sequence GK-677G09-023107,
 genomic survey sequence.

ACCESSION

BX661683
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Arabidopsis thaliana (thale cress)

Eukaryota

Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1
 Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana

JOURNAL

MECLINE
 PUBMED
 REFERENCE
 AUTHORS
 Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
 Weisshaar,B.

TITLE

An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 flanking sequence tag-based reverse genetics
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)

JOURNAL

MECLINE
 PUBMED
 REFERENCE
 AUTHORS
 Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
 Weisshaar,B.

TITLE

High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 Biotechniques 35 (6), 1164-1168 (2003)

JOURNAL

PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion within the locus defined by BAC clone
 MGD8. Details on the protocols used for generation of the sequence
 are described in References 1-3. The sequences are generated at the
 MPI for Plant Breeding Research in the context of the GABI-Kat
 project. GABI-Kat is part of the German Plant Genomics program
 designated "GABI". Information on line availability can be found
 at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

Location/Qualifiers

1..49
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-677G09-023107"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161 (Genbank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."

ORIGIN

Query Match 60.0%; Score 12; DB 9; Length 49;

Best Local Similarity 55.0%; Pred. No. 4.7e+05;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAUGCCUU 20
|||||:|:|:|:
Db 5 AACGGAGGCTGCTTCTT 24

RESULT 23

N50146

LOCUS

DEFINITION y12f02.s1 Soares multiple sclerosis 2NbHSP Homo sapiens cDNA
Clone IMAGE:282843 3' similar to gb:f02932 PEROXISOME PROLIFERATOR
ACTIVATED RECEPTOR ALPHA (HUMAN); mRNA sequence.

ACCESSION N50146

VERSION N50146.1

KEYWORDS GI:1191312

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 36)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Rultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasaki, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ml3 -40 forward

High quality sequence stop: 1.

FEATURES

source

1..36
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3901371"

/db_xref="taxon:9606"

/clone="IMAGE:282843"

/sex="male"

/tissue_type="multiple sclerosis lesions"

/dev_stage="Age 46"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares multiple sclerosis 2NbHSP"

/note="Vector: p7T73D (Pharmacia) with a modified

Folylinker V-TYPE: phagemid; Site 1: Not I; Site 2: Eco

RI; 1st strand cDNA was primed with a Not I - oligo(dT)

Primer [5',

TGTACCAATCTGAAGTGGGCGCGCATTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified p7T73 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis

lesions from one patient was kindly provided by Dr. Kevin

G. Becker (NINDS/NIH)."

ORIGIN

Query Match

Best Local Similarity 59.0%; Score 11.8; DB 7; Length 36;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GGAGGCTGGGAAGTC 18

|||||:|:|:|:

Db 8 GGAGGCTGGGAAGTC 22

RESULT 24

CC326042/c

LOCUS

DEFINITION

CC326042 42 bp mRNA linear GSS 03-OCT-2003.
RST753 BayGenomics Gene Trap Library pGT0TMPfs Mus musculus cDNA,
mRNA sequence.

ACCESSION CC326042

VERSION CC326042.2

KEYWORDS GI:37500541

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 42)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

BayGenomics.
http://baygenomics.ucsf.edu/

JOURNAL Unpublished (2001)

COMMENT On Oct 3, 2003 this sequence version replaced gi:30720100.

Contact: BayGenomics

Bay Area Functional Genomics Consortium (BayGenomics)

Email: info@baygenomics.ucsf.edu

Sequence tag generated by 5' RACE of total RNA from gene trap ES

cell line. ES cell lines harboring insertion mutation of target

gene are available upon request from BayGenomics. Annotation

information available from

http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=

CELL_LINE&KEY=RST753

Class: Gene Trap.

Location/Qualifiers

1..42

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129 Ola"

/db_xref="taxon:10090"

/sex="Male"

/cell_type="Embryonic stem cell"

/clone_lib="BayGenomics Gene Trap Library pGT0TMPfs"

/note="Vector: pGT0TMPfs"

ORIGIN

Query Match

Best Local Similarity 59.0%; Score 11.8; DB 8; Length 42;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGGAGGCTGGGAAGC 17

|||||:|:|:|:

Db 20 CGGAGGCTGGGAAGC 6

RESULT 25

AZ603333/c

LOCUS

DEFINITION

AZ603333 47 bp DNA linear GSS 13-DEC-2000
IM0422D14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0422D14 R, genomic survey sequence.

ACCESSION AZ603333

VERSION AZ603333.1

KEYWORDS GI:11725619

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 47)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Isaiah, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0422 row: D column: 14
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 47.

FEATURES

source

1. .47

Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0422D14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 59.0%; Score 11.8; DB 8; Length 47;
Best Local Similarity 73.3%; Pred. NO. 5.8e+05;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GGAGGCTGGGGAUCC 18
Db 28 GGAGGCTGGGCTTCC 14

Search completed: May 24, 2005, 11:42:05
Job time : 3004 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 08:34:01 ; Search time 125 Seconds
(without alignments)
261.804 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacggaggcgggaugccu 20

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

Issued Patents_NA.*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.8	74.0	29	4	US-09-968-362A-5
C 2	14.8	74.0	29	4	US-09-968-362A-6
C 3	14.4	72.0	26	4	US-09-496-118B-11
C 4	13.8	69.0	22	3	US-09-462-606-19
C 5	13.8	69.0	25	4	US-09-396-196G-24579
C 6	13.8	69.0	25	4	US-09-396-196G-24580
C 7	13.8	69.0	25	4	US-09-396-196G-24581
C 8	13.8	69.0	25	4	US-09-396-196G-24582
C 9	13.8	69.0	25	4	US-09-396-196G-24583
C 10	13.6	68.0	38	1	US-08-106-761-12
C 11	13.6	68.0	50	3	US-08-937-195-17
C 12	13.6	68.0	50	3	US-08-937-195-17
C 13	13.6	68.0	50	5	US-08-937-195-17
C 14	13.2	66.0	20	3	US-09-167-921-45
C 15	13.2	66.0	20	3	US-09-277-020-47
C 16	13.2	66.0	20	3	US-09-321-743-45
C 17	13.2	66.0	20	3	US-09-396-196G-107681
C 18	13.2	66.0	20	4	US-09-705-267A-28
C 19	13.2	66.0	20	4	US-09-367-007C-26
C 20	12.8	64.0	25	4	US-09-396-196G-24578
C 21	12.8	64.0	25	4	US-09-396-196G-24584
C 22	12.8	64.0	26	5	US-09-396-196G-24584
C 23	12.6	63.0	25	4	US-09-396-196G-14290
C 24	12.6	63.0	36	3	US-08-501-253A-6
C 25	12.6	63.0	47	4	US-09-422-978-1920
C 26	12.4	62.0	18	3	US-09-339-964-36
C 27	12.4	62.0	20	4	US-09-060-299-266

28	12.4	62.0	20	4	US-09-402-923A-266	Sequence 266, App
29	12.4	62.0	21	3	US-09-177-650-59	Sequence 59, Appl
30	12.4	62.0	21	4	US-09-984-316A-10	Sequence 10, Appl
C 31	12.4	62.0	29	4	US-09-304-232-315	Sequence 315, App
C 32	12.4	62.0	40	4	US-09-060-299-267	Sequence 267, App
C 33	12.4	62.0	40	4	US-09-402-923A-267	Sequence 267, App
C 34	12.2	61.0	19	3	US-08-766-528-50	Sequence 50, Appl
C 35	12.2	61.0	19	4	US-09-661-858-50	Sequence 50, Appl
C 36	12.2	61.0	24	3	US-08-755-187-165	Sequence 165, App
C 37	12.2	61.0	25	4	US-09-396-196G-14587	Sequence 14587, A
C 38	12.2	61.0	25	4	US-09-396-196G-38506	Sequence 38506, A
C 39	12.2	61.0	25	4	US-09-396-196G-38506	Sequence 38506, A
C 40	12.2	61.0	25	4	US-09-396-196G-63055	Sequence 63055, A
C 41	12.2	61.0	26	3	US-09-485-737B-63	Sequence 63, Appl
C 42	12.2	61.0	26	3	US-09-485-737B-63	Sequence 63, Appl
C 43	12.2	61.0	26	4	US-10-071-485-63	Sequence 63, Appl
C 44	12.2	61.0	26	4	US-10-071-485-63	Sequence 63, Appl
C 45	12.2	61.0	28	3	US-09-526-935B-7	Sequence 7, Appl
C 46	12.2	61.0	28	4	US-09-880-887A-7	Sequence 7, Appl
C 47	12.2	61.0	36	4	US-09-864-866-39	Sequence 39, Appl
C 48	12	60.0	20	3	US-09-357-071-40	Sequence 40, Appl
C 49	12	60.0	20	4	US-10-087-229-2	Sequence 2, Appl
C 50	12	60.0	25	1	US-08-411-796-46	Sequence 46, Appl
C 51	12	60.0	25	3	US-08-471-039-46	Sequence 46, Appl
C 52	12	60.0	25	4	US-08-539-390-46	Sequence 46, Appl
C 53	12	60.0	25	4	US-09-396-196G-5726	Sequence 5726, A
C 54	12	60.0	25	4	US-09-396-196G-60290	Sequence 60290, A
C 55	12	60.0	25	4	US-09-396-196G-107633	Sequence 107633, A
C 56	12	60.0	25	5	PCT-US93-11198-46	Sequence 46, Appl
C 57	12	60.0	26	1	US-08-411-796-465	Sequence 465, App
C 58	12	60.0	26	3	US-08-471-039-465	Sequence 465, App
C 59	12	60.0	26	4	US-08-559-390-465	Sequence 465, App
C 60	12	60.0	27	5	PCT-US93-11198-465	Sequence 465, App
C 61	12	60.0	27	3	US-08-567-200A-22	Sequence 22, Appl
C 62	12	60.0	27	3	US-08-631-794-25	Sequence 25, Appl
C 63	12	60.0	33	1	US-08-217-082A-4	Sequence 4, Appl
C 64	12	60.0	33	2	US-08-465-485A-4	Sequence 4, Appl
C 65	12	60.0	33	3	US-09-080-285-4	Sequence 4, Appl
C 66	12	60.0	33	3	US-09-724-426-4	Sequence 4, Appl
C 67	12	60.0	38	1	US-08-093-741-56	Sequence 56, Appl
C 68	12	60.0	38	1	US-08-720-012-56	Sequence 56, Appl
C 69	12	60.0	39	1	US-07-781-254A-12	Sequence 12, Appl
C 70	11.8	59.0	20	3	US-09-444-053-44	Sequence 44, Appl
C 71	11.8	59.0	21	3	US-09-045-054-28	Sequence 28, Appl
C 72	11.8	59.0	25	4	US-09-396-196G-1898	Sequence 1898, Ap
C 73	11.8	59.0	25	4	US-09-396-196G-47272	Sequence 47272, A
C 74	11.8	59.0	25	4	US-09-396-196G-75117	Sequence 75117, A
C 75	11.8	59.0	25	4	US-09-396-196G-78712	Sequence 78712, A
C 76	11.8	59.0	25	4	US-09-396-196G-78712	Sequence 78712, A
C 77	11.8	59.0	25	4	US-09-396-196G-87612	Sequence 87612, A
C 78	11.8	59.0	25	4	US-09-396-196G-108158	Sequence 108158, A
C 79	11.8	59.0	25	4	US-09-396-196G-108159	Sequence 108159, A
C 80	11.8	59.0	26	4	US-09-396-196G-122781	Sequence 122781, A
C 81	11.8	59.0	26	4	US-09-268-311-9	Sequence 9, Appl
C 82	11.8	59.0	26	4	US-09-154-219-9	Sequence 9, Appl
C 83	11.8	59.0	27	2	US-08-735-609-7	Sequence 7, Appl
C 84	11.8	59.0	27	2	US-08-735-609-7	Sequence 7, Appl
C 85	11.8	59.0	27	3	US-09-315-372-7	Sequence 7, Appl
C 86	11.8	59.0	27	3	US-09-244-752-7	Sequence 7, Appl
C 87	11.8	59.0	27	3	US-09-245-497-7	Sequence 7, Appl
C 88	11.8	59.0	27	3	US-09-562-919-7	Sequence 7, Appl
C 89	11.8	59.0	28	4	US-09-268-311-11	Sequence 11, Appl
C 90	11.8	59.0	28	4	US-09-268-311-11	Sequence 11, Appl
C 91	11.8	59.0	28	4	US-09-154-219-11	Sequence 11, Appl
C 92	11.8	59.0	28	4	US-09-154-219-11	Sequence 11, Appl
C 93	11.8	59.0	30	2	US-08-713-939A-66	Sequence 66, Appl
C 94	11.8	59.0	30	2	US-08-422-333-25	Sequence 25, Appl
C 95	11.8	59.0	30	3	US-09-036-579-66	Sequence 66, Appl
C 96	11.8	59.0	30	3	US-09-550-374-66	Sequence 66, Appl
C 97	11.8	59.0	30	4	US-09-943-506-66	Sequence 66, Appl
C 98	11.8	59.0	36	1	US-08-325-553-32	Sequence 32, Appl
C 99	11.8	59.0	36	1	US-08-325-553-33	Sequence 33, Appl
C 100	11.8	59.0	36	2	US-08-394-152A-32	Sequence 32, Appl

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101 11.8 59.0 36 2 US-08-394-152A-33 Sequence 33, Appl
c 102 11.8 59.0 36 4 US-08-705-477E-32 Sequence 32, Appl
103 11.8 59.0 36 4 US-08-705-477E-33 Sequence 33, Appl
c 104 11.8 59.0 40 3 US-09-171-945-129 Sequence 129, App
105 11.8 59.0 47 4 US-09-422-978-270 Sequence 270, App
c 106 11.8 59.0 48 1 US-08-411-796-165 Sequence 165, App
c 107 11.8 59.0 48 3 US-08-471-039-165 Sequence 165, App
c 108 11.8 59.0 48 4 US-08-559-390-165 Sequence 165, App
c 109 11.8 59.0 48 5 PCT-US93-11198-165 Sequence 165, App
c 110 11.6 58.0 20 4 US-09-575-081B-20 Patent No. 5219727
c 111 11.6 58.0 20 6 5219727-7 Patent No. 5219727
c 112 11.6 58.0 20 6 5219727-7 Patent No. 5219727
c 113 11.6 58.0 21 1 US-08-445-050-21 Sequence 21, Appl
c 114 11.6 58.0 21 1 US-08-204-691-21 Sequence 21, Appl
c 115 11.6 58.0 24 2 US-08-859-998-893 Sequence 893, App
c 116 11.6 58.0 24 3 US-09-225-928-893 Sequence 893, App
c 117 11.6 58.0 24 4 US-09-225-201B-893 Sequence 893, App
c 118 11.6 58.0 25 4 US-09-396-196G-7312 Sequence 7312, App
c 119 11.6 58.0 25 4 US-09-396-196G-14809 Sequence 14809, A
c 120 11.6 58.0 25 4 US-09-396-196G-44392 Sequence 44392, A
c 121 11.6 58.0 25 4 US-09-396-196G-44393 Sequence 44393, A
c 122 11.6 58.0 25 4 US-09-396-196G-44394 Sequence 44394, A
c 123 11.6 58.0 25 4 US-09-396-196G-44409 Sequence 44409, A
c 124 11.6 58.0 25 4 US-09-396-196G-49130 Sequence 49130, A
c 125 11.6 58.0 25 4 US-09-396-196G-59215 Sequence 59215, A
c 126 11.6 58.0 25 4 US-09-396-196G-72971 Sequence 72971, A
c 127 11.6 58.0 25 4 US-09-396-196G-78207 Sequence 78207, A
c 128 11.6 58.0 25 4 US-09-396-196G-109238 Sequence 109238, A
c 129 11.6 58.0 27 2 US-08-479-275D-6 Sequence 6, Appl
c 130 11.6 58.0 27 2 US-08-488-271B-6 Sequence 6, Appl
c 131 11.6 58.0 27 3 US-09-194-842A-37 Sequence 37, Appl
c 132 11.6 58.0 30 1 US-08-437-815-8 Sequence 8, Appl
c 133 11.6 58.0 30 1 US-08-897-040-8 Sequence 8, Appl
c 134 11.6 58.0 31 4 US-09-155-327G-3 Sequence 3, Appl
c 135 11.6 58.0 32 3 US-08-577-081A-28 Sequence 28, Appl
c 136 11.6 58.0 32 3 US-08-577-081A-35 Sequence 35, Appl
c 137 11.6 58.0 33 3 US-08-567-200A-21 Sequence 21, Appl
c 138 11.6 58.0 33 3 US-08-691-794-24 Sequence 24, Appl
c 139 11.6 58.0 36 1 US-08-451-715A-27 Sequence 27, Appl
c 140 11.6 58.0 40 3 US-09-522-217-53 Sequence 53, Appl
c 141 11.6 58.0 40 4 US-09-523-246-53 Sequence 53, Appl
c 142 11.6 58.0 40 4 US-10-295-723-53 Sequence 53, Appl
c 143 11.6 58.0 45 1 US-08-171-389-110 Sequence 110, App
c 144 11.6 58.0 45 1 US-08-123-936-110 Sequence 110, App
c 145 11.6 58.0 45 2 US-08-475-228A-110 Sequence 110, App
c 146 11.6 58.0 45 3 US-08-482-080A-110 Sequence 110, App
c 147 11.6 58.0 45 3 US-09-354-947-110 Sequence 110, App
c 148 11.6 58.0 45 5 PCT-US93-12388-110 Sequence 110, App
c 149 11.4 57.0 18 1 US-08-363-240A-1105 Sequence 1105, App
c 150 11.4 57.0 18 4 US-09-422-978-7891 Sequence 7891, App
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ALIGNMENTS

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RESULT 1
US-09-968-362A-5
; Sequence 5, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION: increased biological activities
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: FC fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-968-362A-5
Query Match 74.0%; Score 14.8; DB 4; Length 29;
Best Local Similarity 77.8%; Pred. No. 5.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 2 ACGGAGGCGCGGAGCCU 19
Db 12 ATGGAGGCTGGAGGCCT 29
RESULT 2
US-09-968-362A-6/c
; Sequence 6, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: FC fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-968-362A-6
Query Match 74.0%; Score 14.8; DB 4; Length 29;
Best Local Similarity 77.8%; Pred. No. 5.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 2 ACGGAGGCGCGGAGCCU 19
Db 18 ATGGAGGCTGGAGGCCT 1
RESULT 3
US-09-496-118B-11/c
; Sequence 11, Application US/09496118B
; Patent No. 6475986
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, Bharat B.
; TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates
; FILE REFERENCE: D6206
; CURRENT APPLICATION NUMBER: US/09/496,118B
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: US 60/118,531
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 11
; LENGTH: 26
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: primer bind
; OTHER INFORMATION: PCR primer used for amplifying the cDNA encoding
; OTHER INFORMATION: the extracellular domain of THANK
US-09-496-118B-11
Query Match 72.0%; Score 14.4; DB 4; Length 26;
Best Local Similarity 81.2%; Pred. No. 8.3e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Qy 3 CCGAGGCGUGGAUCC 18
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Db 18 CCGAGGCTGGATGCC 3

RESULT 4

US-09-462-606-19/c
; Sequence 19, Application US/09462606
; Patent No. 6432408
; GENERAL INFORMATION:
; APPLICANT: MENG, XIANG-JIN
; APPLICANT: Emerson, Suzanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS AND USES THEREOF
; FILE REFERENCE: 20264267US1
; CURRENT APPLICATION NUMBER: US/09/462,606
; CURRENT FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 60/053069
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/14665
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Hepatitis E virus
US-09-462-606-19

Query Match 69.0%; Score 13.8; DB 3; Length 22;
Best Local Similarity 68.4%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAUCCU 19
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Db 22 AATGAAGCTGGAAGCCT 4

RESULT 5

US-09-396-196G-24579/c
; Sequence 24579, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24579
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24579

Query Match 69.0%; Score 13.8; DB 4; Length 25;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAUCC 17
|||||:||||: ||
Db 25 AACTGAGGCTGTGATGC 9

RESULT 6

US-09-396-196G-24580/c

; Sequence 24580, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24580
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24580

Query Match 69.0%; Score 13.8; DB 4; Length 25;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAUCC 17
|||||:||||: ||
Db 23 AACTGAGGCTGTGATGC 7

RESULT 7

US-09-396-196G-24581/c
; Sequence 24581, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24581
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24581

Query Match 69.0%; Score 13.8; DB 4; Length 25;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAUCC 17
|||||:||||: ||
Db 20 AACTGAGGCTGTGATGC 4

RESULT 8

US-09-396-196G-24582/c
; Sequence 24582, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1

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; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24582
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24582

Query Match      69.0%; Score 13.8; DB 4; Length 25;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGCGGCGGGAUGC 17
Db 19 AACTGAGCGTGTGATGC 3

RESULT 9
US-09-396-196G-24583/c
; Sequence 24583, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24583
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24583

Query Match      69.0%; Score 13.8; DB 4; Length 25;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGCGGCGGGAUGC 17
Db 17 AACTGAGCGTGTGATGC 1

RESULT 10
US-08-106-761-12/c
; Sequence 12, Application US/08106761
; Patent No. 5445956
; GENERAL INFORMATION:
; APPLICANT: HAMMOCK, Bruce D.
; APPLICANT: GRANT, David F.
; APPLICANT: BEETHAM, Jeffrey K.
; TITLE OF INVENTION: RECOMBINANT SOLUBLE EPOXIDE HYDROLASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW
; STREET: Steuart Street Tower, 20th Floor, One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk

; CURRENT APPLICATION NUMBER: US/08/937,195
; CURRENT FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 2307E-445
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-106-761-12

Query Match      68.0%; Score 13.6; DB 1; Length 38;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGCGGCGGGAUCCUU 20
Db 30 AGCAGAGATTGGGATGCCTT 11

RESULT 11
US-08-937-195-17
; Sequence 17, Application US/08937195
; Patent No. 6136561
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,195
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/488,807
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 17:
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; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US96-07627-17

Query Match 68.0%; Score 13.6; DB 5; Length 50;
Best Local Similarity 70.0%; Pred. NO. 2.2e+03;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGGAUGCCUU 20
Db 20 AAGGGAGCGCGGATGTCAT 39

RESULT 14
US-09-167-921-45/c
; Sequence 45, Application US/09167921A
; Patent No. 6172216
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0324
; CURRENT APPLICATION NUMBER: US/09/167,921A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-167-921-45

Query Match 66.0%; Score 13.2; DB 3; Length 20;
Best Local Similarity 61.1%; Pred. NO. 3.1e+03;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGGAGCGCGGGAUGCCUU 20
Db 20 CGGCGGCTGGGATCTTT 3

RESULT 15
US-09-277-020-47/c
; Sequence 47, Application US/09277020
; Patent No. 6210892
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
; FILE REFERENCE: ISPH-0339
; CURRENT APPLICATION NUMBER: US/09/277,020
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/167,921

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Best Local Similarity 84.6%; Pred. No. 4e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGGCGUGGAGCC 18
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Db 10 AGGTGGGATGCC 22

RESULT 20

US-09-396-196G-24578/c
; Sequence 24578, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24578
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24578

Query Match 64.0%; Score 12.8; DB 4; Length 25;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGCGGCGGAGCC 17
| | | | | | | | | |
Db 25 ACTGAGGCTGTGATGC 10

RESULT 21

US-09-396-196G-24584/c
; Sequence 24584, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24584
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24584

Query Match 64.0%; Score 12.8; DB 4; Length 25;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGAGGCGGAGG 16
| | | | | | | | | |
Db 16 AACTGAGGCTGTGATG 1

RESULT 22

Query Match 64.0%; Score 12.8; DB 5; Length 26;
Best Local Similarity 87.5%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

PCT-US92-06821A-27
; Sequence 27, Application PC/TUS9206821A
; GENERAL INFORMATION:
; APPLICANT: Shah, Jyotsna S.
; APPLICANT: Nietupski, Raymond M.
; APPLICANT: Liu, Jing
; TITLE OF INVENTION: Oligonucleotides Complementary to
; TITLE OF INVENTION: Mycobacterial Nucleic Acids
; NUMBER OF SEQUENCES: 133
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corporation
; STREET: 200 East Randolph Drive, P.O. Box 87703
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06821A
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/744,282
; FILING DATE: 13-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, Norval B.
; REGISTRATION NUMBER: 33,595
; REFERENCE/DOCKET NUMBER: CN 5851
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-856-7180
; TELEFAX: 312-856-4972
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
PCT-US92-06821A-27

Query Match 64.0%; Score 12.8; DB 5; Length 26;
Best Local Similarity 87.5%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GGAGGCGGAGGCGCC 19
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Db 1 GGAGGCGGAGGCGCC 16

RESULT 23

US-09-396-196G-14290
; Sequence 14290, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14290
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-14290

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Query Match      63.0%; Score 12.6; DB 4; Length 25;
Best Local Similarity 68.4%; Pred. No. 6.3e+03;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCU 19
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Db 7 AACGGGCGCTGGGACACTT 25

RESULT 24
US-08-501-253A-6
; Sequence 6, Application US/08501253A
; Patent No. 6146628
; GENERAL INFORMATION:
; APPLICANT: Uckun, Fatih
; TITLE OF INVENTION: Biotherapeutic Agents Comprising
; TITLE OF INVENTION: Recombinant PAP and PAP Mutants
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 6146628west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: US
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/501,253A
; FILING DATE: 11-JUL-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettleberger, Denise M.
; REGISTRATION NUMBER: 33,924
; REFERENCE/DOCKET NUMBER: 600.323US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-501-253A-6

Query Match      63.0%; Score 12.6; DB 3; Length 36;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACGGAGGCGUGGAUGCCU 20
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Db 17 ACGGAGACTGAGGTCCTT 35

RESULT 25
US-09-422-978-1920/c
; Sequence 1920, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
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; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1920
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-7356-176 : polymorphic base A or G
US-09-422-978-1920

Query Match      63.0%; Score 12.6; DB 4; Length 47;
Best Local Similarity 73.7%; Pred. No. 6.6e+03;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCU 19
    ||||| |||:|||||
Db 46 AAGGGAGGAGGGGAGGCCT 28

Search completed: May 24, 2005, 11:44:11
Job time : 131 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 10:21:35 ; Search time 517 Seconds
(without alignments)
237.227 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacggaggcgggaugccu 20

Scoring table: IDENTITY NUC

Gapop 10'0 , Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 5377818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Published Applications NA:*

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18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10F_NEW_PUB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	†				
C 1	17	85.0		20	17	US-10-422-466-55	Sequence 55, Appl
C 2	15.2	76.0		20	16	US-10-365-623-21	Sequence 21, Appl
C 3	15.2	76.0		25	19	US-10-719-900-75269	Sequence 75269, A
C 4	14.8	74.0		25	19	US-10-719-900-350318	Sequence 350318,
C 5	14.8	74.0		29	10	US-09-968-362-5	Sequence 5, Appl
C 6	14.8	74.0		29	10	US-09-968-362-6	Sequence 6, Appl
C 7	14.8	74.0		29	10	US-09-932-812-5	Sequence 5, Appl
C 8	14.8	74.0		29	10	US-09-932-812-6	Sequence 6, Appl
C 9	14.8	74.0		29	18	US-10-761-593A-5	Sequence 5, Appl
C 10	14.8	74.0		29	18	US-10-761-593A-6	Sequence 6, Appl
C 11	14.8	74.0		29	18	US-10-800-497-5	Sequence 5, Appl

85	12.6	63.0	25	15	US-10-098-263B-15332	Sequence 15332, A
86	12.6	63.0	25	18	US-10-717-597-1299	Sequence 1299, Ap
87	12.6	63.0	25	19	US-10-719-900-61437	Sequence 61437, A
88	12.6	63.0	25	19	US-10-719-900-99273	Sequence 99273, A
89	12.6	63.0	25	19	US-10-719-900-119719	Sequence 119719,
90	12.6	63.0	25	19	US-10-719-900-129747	Sequence 129747,
91	12.6	63.0	25	19	US-10-719-900-149406	Sequence 149406,
92	12.6	63.0	25	19	US-10-719-900-254549	Sequence 254549,
93	12.6	63.0	25	19	US-10-719-900-254550	Sequence 254550,
94	12.6	63.0	25	19	US-10-719-900-264754	Sequence 264754,
95	12.6	63.0	25	19	US-10-719-900-264756	Sequence 264756,
96	12.6	63.0	25	19	US-10-719-900-277708	Sequence 277708,
97	12.6	63.0	25	19	US-10-719-900-298797	Sequence 298797,
98	12.6	63.0	25	19	US-10-719-900-409301	Sequence 409301,
99	12.6	63.0	25	19	US-10-719-900-473336	Sequence 473336,
100	12.6	63.0	25	19	US-10-719-900-644072	Sequence 644072,
101	12.6	63.0	25	19	US-10-719-900-760233	Sequence 760233,
102	12.6	63.0	25	19	US-10-719-900-847343	Sequence 847343,
103	12.6	63.0	25	19	US-10-719-900-917152	Sequence 917152,
104	12.6	63.0	25	19	US-10-809-189-14290	Sequence 14290, A
105	12.6	63.0	27	19	US-10-872-681-8	Sequence 8, Appli
106	12.6	63.0	31	9	US-09-801-274-1444	Sequence 1444, Ap
107	12.6	63.0	40	17	US-10-260-238-6006	Sequence 6006, Ap
108	12.6	63.0	42	14	US-10-008-063-23	Sequence 23, Appl
109	12.6	63.0	42	15	US-10-152-363A-13	Sequence 13, Appl
110	12.6	63.0	47	17	US-10-349-143-1920	Sequence 1920, Ap
111	12.6	63.0	50	17	US-10-131-827-4596	Sequence 4596, Ap
112	12.4	62.0	20	16	US-10-331-907-266	Sequence 266, App
113	12.4	62.0	21	9	US-09-984-316A-10	Sequence 10, Appl
114	12.4	62.0	21	16	US-10-096-578-59	Sequence 59, Appl
115	12.4	62.0	23	16	US-10-230-381-32	Sequence 32, Appl
116	12.4	62.0	25	15	US-10-098-263B-64540	Sequence 64540, A
117	12.4	62.0	25	19	US-10-719-900-60664	Sequence 60664, A
118	12.4	62.0	25	19	US-10-719-900-248034	Sequence 248034,
119	12.4	62.0	25	19	US-10-719-900-392535	Sequence 392535,
120	12.4	62.0	25	19	US-10-719-900-392536	Sequence 392536,
121	12.4	62.0	25	19	US-10-719-900-403549	Sequence 403549,
122	12.4	62.0	25	19	US-10-719-900-429574	Sequence 429574,
123	12.4	62.0	25	19	US-10-719-900-443150	Sequence 443150,
124	12.4	62.0	25	19	US-10-719-900-473856	Sequence 473856,
125	12.4	62.0	25	19	US-10-719-900-622593	Sequence 622593,
126	12.4	62.0	25	19	US-10-719-900-622599	Sequence 622599,
127	12.4	62.0	25	19	US-10-719-900-622601	Sequence 622601,
128	12.4	62.0	25	19	US-10-719-900-640210	Sequence 640210,
129	12.4	62.0	25	19	US-10-719-900-751582	Sequence 751582,
130	12.4	62.0	25	19	US-10-719-900-777938	Sequence 777938,
131	12.4	62.0	25	19	US-10-719-900-844928	Sequence 844928,
132	12.4	62.0	25	19	US-10-719-900-868764	Sequence 868764,
133	12.4	62.0	25	19	US-10-719-900-914921	Sequence 914921,
134	12.4	62.0	25	19	US-10-719-900-936355	Sequence 936355,
135	12.4	62.0	27	16	US-10-289-757-201	Sequence 201, App
136	12.4	62.0	29	16	US-10-336-638-315	Sequence 315, App
137	12.4	62.0	31	9	US-09-801-274-1558	Sequence 1558, Ap
138	12.4	62.0	37	9	US-09-981-393-5	Sequence 5, Appli
139	12.4	62.0	37	18	US-10-627-588-5	Sequence 5, Appli
140	12.4	62.0	40	16	US-10-331-907-267	Sequence 267, App
141	12.4	62.0	50	17	US-10-131-827-5741	Sequence 5741, Ap
142	12.2	61.0	19	18	US-10-723-552-50	Sequence 50, Appl
143	12.2	61.0	19	19	US-10-783-128-353	Sequence 353, App
144	12.2	61.0	19	19	US-10-783-128-354	Sequence 354, App
145	12.2	61.0	19	19	US-10-783-128-355	Sequence 355, App
146	12.2	61.0	19	19	US-10-783-128-2105	Sequence 2105, Ap
147	12.2	61.0	19	19	US-10-783-128-2106	Sequence 2106, Ap
148	12.2	61.0	19	19	US-10-783-128-2107	Sequence 2107, Ap
149	12.2	61.0	20	15	US-10-007-078-42	Sequence 42, Appl
150	12.2	61.0	21	18	US-10-751-736-53290	Sequence 53290, A

ALIGNMENTS

RESULT 3
US-10-719-900-75269
; Sequence 75269, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou

; Sequence 55, Application US/10422466
; Publication No. US2004006036A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Ji-Fan
; APPLICANT: Bowersox, Scott
; TITLE OF INVENTION: Silencing transcription by methylation
; FILE REFERENCE: 112029.00005
; CURRENT APPLICATION NUMBER: US/10/422,466
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: 09/643,128
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 60/196,749
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/214,148
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (19)
; OTHER INFORMATION: m5c at base 19
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor
US-10-422-466-55

Query Match 85.0%; Score 17; DB 17; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.2e+02;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGAGGCGUGGCGGC 17
DB 17 AACGAGGCGGCGATGC 1
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RESULT 2
US-10-365-623-21/c
; Sequence 21, Application US/10365623
; Publication No. US20030166512A1
; GENERAL INFORMATION:
; APPLICANT: Xie, Dong
; TITLE OF INVENTION: Protein Carrier System for Therapeutic Oligonucleotides
; FILE REFERENCE: 63024.000001
; CURRENT APPLICATION NUMBER: US/10/365,623
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MB-003 antisense oligonucleotide
US-10-365-623-21

Query Match 76.0%; Score 15.2; DB 16; Length 20;
Best Local Similarity 65.0%; Pred. No. 1.6e+03;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 AACGAGGCGUGGCGCCUU 20
DB 20 AACGCGGCGTGGGATACTTT 1
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RESULT 8
US-09-932-812-6/c
; Sequence 6, Application US/09932812
; Publication No. US20030082749A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-932-812-6

Query Match          74.0%;      Score 14.8;  DB 10;  Length 29;
Best Local Similarity 77.8%;      Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGCGCGGAGCCU 19
Db 18 ATGGAGGCTGGGAGCCT 1

RESULT 9
US-10-761-593A-5
; Sequence 5, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(29)
; OTHER INFORMATION: synthetic
US-10-761-593A-5

Query Match          74.0%;      Score 14.8;  DB 18;  Length 29;
Best Local Similarity 77.8%;      Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGCGCGGAGCCU 19
Db 12 ATGGAGGCTGGGAGCCT 29

RESULT 10
US-10-761-593A-6/c
; Sequence 6, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:

```

; APPLICANT: Sun, Cecily R
 ; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-
 ; TITLE OF INVENTION: stimulating factor with
 ; TITLE OF INVENTION: increased biological activities
 ; FILE REFERENCE: 03JUN2001
 ; CURRENT APPLICATION NUMBER: US/10/800,497
 ; PRIOR FILING DATE: 2004-03-15
 ; PRIOR FILING DATE: US/09/968,362
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 29
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR primer
 US-10-800-497-6

Query Match 74.0%; Score 14.8; DB 18; Length 29;
 Best Local Similarity 77.8%; Pred. No. 2.4e+03;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCTGGGAGCCU 19
 Db 18 ATGGAGGCTGGGAGCCCT 1

RESULT 13

US-10-800-449-5
 ; Sequence 5, Application US/10800449
 ; Publication No. US20040265973A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sun, Lee-Hwei K
 ; APPLICANT: Sun, Bill
 ; APPLICANT: Sun, Cecily R
 ; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
 ; TITLE OF INVENTION: increased biological activities
 ; FILE REFERENCE: 03JUN2001
 ; CURRENT APPLICATION NUMBER: US/10/800,449
 ; CURRENT FILING DATE: 2004-03-15
 ; PRIOR APPLICATION NUMBER: US/09/968,362
 ; PRIOR FILING DATE: 2001-10-01
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 29
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR primer
 US-10-800-449-5

Query Match 74.0%; Score 14.8; DB 18; Length 29;
 Best Local Similarity 77.8%; Pred. No. 2.4e+03;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCTGGGAGCCU 19
 Db 12 ATGGAGGCTGGGAGCCCT 29

RESULT 14

US-10-800-449-6/c
 ; Sequence 6, Application US/10800449
 ; Publication No. US20040265973A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sun, Lee-Hwei K
 ; APPLICANT: Sun, Bill
 ; APPLICANT: Sun, Cecily R
 ; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
 ; TITLE OF INVENTION: increased biological activities
 ; FILE REFERENCE: 03JUN2001

; CURRENT APPLICATION NUMBER: US/10/800,449
 ; CURRENT FILING DATE: 2004-03-15
 ; PRIOR APPLICATION NUMBER: US/09/968,362
 ; PRIOR FILING DATE: 2001-10-01
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 29
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR primer
 US-10-800-449-6

Query Match 74.0%; Score 14.8; DB 18; Length 29;
 Best Local Similarity 77.8%; Pred. No. 2.4e+03;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCTGGGAGCCU 19
 Db 18 ATGGAGGCTGGGAGCCCT 1

RESULT 15

US-09-740-332-204/c
 ; Sequence 204, Application US/09740332
 ; Publication No. US20030125270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals Inc.
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
 ; TITLE OF INVENTION: Hepatitis C Virus Infection
 ; FILE REFERENCE: RPI 400/003
 ; CURRENT APPLICATION NUMBER: US/09/740,332
 ; CURRENT FILING DATE: 2001-03-26
 ; NUMBER OF SEQ ID NOS: 9704
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 204
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION:
 ; OTHER INFORMATION: oligonucleotide substrate
 US-09-740-332-204

Query Match 72.0%; Score 14.4; DB 10; Length 17;
 Best Local Similarity 81.2%; Pred. No. 3.9e+03;
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGATG 16
 Db 17 ACGGAGGCTGGGATG 2

RESULT 16

US-09-740-332-4351
 ; Sequence 4351, Application US/09740332
 ; Publication No. US20030125270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals Inc.
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
 ; TITLE OF INVENTION: Hepatitis C Virus Infection
 ; FILE REFERENCE: RPI 400/003
 ; CURRENT APPLICATION NUMBER: US/09/740,332
 ; CURRENT FILING DATE: 2001-03-26
 ; NUMBER OF SEQ ID NOS: 9704
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4351
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: artificial sequence
 ; FEATURE:

; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4351

Query Match 72.0%; Score 14.4; DB 10; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUG 16
| | | | | | | | | | | | | | | | | | |
Db 2 AGCGGAGGCGUGGAUG 17

RESULT 17
US-09-817-879-204/c
; Sequence 204, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MH800-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 204
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-204

Query Match 72.0%; Score 14.4; DB 10; Length 17;
Best Local Similarity 81.2%; Pred. No. 3.9e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUG 16
| | | | | | | | | | | | | | | | | | |
Db 17 AGCGGAGGCTGGGATG 2

RESULT 18
US-09-817-879-4351
; Sequence 4351, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MH800-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4351
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4351

Query Match 72.0%; Score 14.4; DB 10; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUG 16
| | | | | | | | | | | | | | | | | | |
Db 2 AGCGGAGGCGUGGAUG 17

RESULT 19
US-10-669-841-2797/c
; Sequence 2797, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Ravco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS C VIRUS
; FILE REFERENCE: 400/042US (WBH02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2797
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-2797

Query Match 72.0%; Score 14.4; DB 18; Length 17;
Best Local Similarity 81.2%; Pred. No. 3.9e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUG 16
| | | | | | | | | | | | | | | | | | |
Db 17 AGCGGAGGCTGGGATG 2

RESULT 20
US-10-669-841-6944
; Sequence 6944, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
APPLICANT: James, McSwiggen
APPLICANT: David, Morrissey
APPLICANT: Pamela, Ravco
APPLICANT: Patrice, Lee
APPLICANT: Kenneth, Draper
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
FILE REFERENCE: 400/042US (WBH802-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: PCT/US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 60/337,055
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 09/817,879
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/740,332
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR FILING DATE: 2000-02-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 16207
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6944
LENGTH: 17
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-6944

Query Match 72.0%; Score 14.4; DB 18; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGGAUG 16
Db 2 AGCGAGGCGUGGGAUG 17

RESULT 21

US-10-170-812-11/c
Sequence 11, Application US/10170812
Publication No. US20030166546A1
GENERAL INFORMATION:
APPLICANT: Aggarwal, Bharat B.
TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates
TITLE OF INVENTION: Apoptosis
FILE REFERENCE: D6206D
CURRENT APPLICATION NUMBER: US/10/170,812
CURRENT FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: US 09/496,118
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 11

LENGTH: 26
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: primer_bind
OTHER INFORMATION: PCR primer used for amplifying the cDNA encoding
OTHER INFORMATION: the extracellular domain of THANK
US-10-170-812-11

US-10-170-812-11

Query Match 72.0%; Score 14.4; DB 16; Length 26;
Best Local Similarity 81.2%; Pred. No. 3.7e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 3 CGGAGGCGUGGGAUGCC 18
Db 18 CGGAGGCTGGGATCCC 3

RESULT 22

US-10-719-900-277707/c
Sequence 277707, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 277707
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-277707

Query Match 71.0%; Score 14.2; DB 19; Length 25;
Best Local Similarity 68.4%; Pred. No. 4.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGGAUGCCU 19
Db 25 ATCAGAGTCTGGGATGCCT 7

RESULT 23

US-10-792-374-10/c
Sequence 10, Application US/10792374
Publication No. US20050079513A1
GENERAL INFORMATION:
APPLICANT: Applied Biosystems
APPLICANT: Lossos, Izidore
APPLICANT: Tibshirani, Rob
APPLICANT: Wechsler, Mark
APPLICANT: Alizadeh, Ash
APPLICANT: Botstein, David
APPLICANT: Levy, Ronald
TITLE OF INVENTION: CLASSIFICATION OF PATIENTS HAVING DIFFUSE LARGE B-CELL LYMPHOMA
TITLE OF INVENTION: BASED UPON GENE EXPRESSION
FILE REFERENCE: 9692-000042
CURRENT APPLICATION NUMBER: US/10/792,374
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 60/510,822
PRIOR FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-10-792-374-10

Query Match 70.0%; Score 14; DB 19; Length 17;
Best Local Similarity 71.4%; Pred. No. 6e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 4;

QY 7 GGCUGGGAGGCCUU 20
|||:||||:|:
Db 17 GGCTGGGATGCCTT 4

RESULT 24
US-10-719-900-622603
; Sequence 622603, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 622603
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-622603

Query Match 70.0%; Score 14; DB 19; Length 25;
Best Local Similarity 71.4%; Pred. No. 5.8e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 4;

QY 7 GGCUGGGAGGCCUU 20
|||:||||:|:
Db 1 GGCTGGGATGCCTT 14

RESULT 25
US-10-719-900-844927/c
; Sequence 844927, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 844927
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-844927

Query Match 70.0%; Score 14; DB 19; Length 25;
Best Local Similarity 71.4%; Pred. No. 5.8e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 4;

QY 7 GGCUGGGAGGCCUU 20
|||:||||:|:
Db 16 GGCTGGGATGCCTT 3